

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gonsalves, Dennis
Meng, Baozhong
- (ii) TITLE OF INVENTION: RUPESTRIS STEM PITTING
ASSOCIATED VIRUS NUCLEIC ACIDS,
PROTEINS, AND THEIR USES
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 - (B) STREET: Clinton Square, P.O. Box 1051
 - (C) CITY: Rochester
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 14603
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/047,147
 - (B) FILING DATE: 20-MAY-1997
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/069,902
 - (B) FILING DATE: 17-DEC-1997
- (ix) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Goldman, Michael L.
 - (B) REGISTRATION NUMBER: 30,727
 - (C) REFERENCE/DOCKET NUMBER: 19603/1722
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (716) 263-1304
 - (B) TELEFAX: (716) 263-1600

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGATAAACAT AACAAACAGAA TCTGCATTGC AGTAATATTC CTTGAATATA ATTGCAACGC	60
AATGGCCCTC TCTTATAGGC CTGCTGTTGA AGAGGTGCTC GCAAAATTCA CCTCTGATGA	120
ACAATCCAGG GTTTCTGCTA CAGCTCTCAA GGCATTAGTA GACTTAGAGG AAAGTCAGCA	180
CAATTTGTTT TCTTTTCGCAT TGCCTGATAG AAGCAAAGAA AGGCTGATAT CTTCTGGCAT	240
TTACTTAAGT CCTTACAGTT TCAGACCCCA CTCACATCCA GTTTGTAAAA CTTTAGAAAA	300
TCACATTTTG TACAATGTTT TACCTAGTTA TGTTAATAAT TCATTTTACT TTGTAGGAAT	360
CAAGGATTTT AAGCTGCAGT TCTTGAAAAG GAGGAATAAG GATCTCAGCT TGGTAGCACT	420
CATAAATAGG TTTGTGACAA GTCGTGATGT TAGTAGGTAT GGGTCTGAGT TCGTTATAAG	480
TTCTAGTGAC AAATCAAGTC AGGTTGTCAG TAGAAAGGGC ATTGGTGATT CTAACACACT	540
CCGGAGATTG GTCCACGTG TAATTTCCAC AGGTGCCAGG AATCTTTTTT TGCATGATGA	600
GATTCACTAC TGGTCAATTA GTGATCTGAT CAATTTTTTT GACGTTGCCA AGCCAAGCAT	660
GCTCTTGCCA ACTGCAGTAA TCCCTCCAGA AGTGCTGGTT GGCTCTCCAG AGAGTCTTAA	720
CCCTTGGGCC TACCAGTATA AAATCAATGG CAACCAACTG CTCTTCGCAC CAGATGGCAA	780
CTGGAATGAG ATGTACTCAC AACCTTTGTC ATGCAGATAC CTGCTCAAGG CCAGATCTGT	840
AGTTCTGCCC GATGGCTCAC GCTACTCGGT TGACATCATT CACTCAAAT TTAGTCACCA	900
CTTGCTTAGT TTCACCCCTA TGGGTAATCT TTTGACTTCA AACATGCGAT GTTTTTCTGG	960
CTTCGATGCA ATAGGCATAA AAGATCTTGA ACCTCTAAGC CGCGGCATGC ACAGTTGCTT	1020
CCCAGTACAT CATGATGTTG TAACTAAGAT ATATCTTTAT TTGAGAACTC TCAAGAAGCC	1080
AGATAAGGAG TCTGCCGAGG CAAAGCTTCG ACAACTCATA GAAAAACCCA CAGGGAGGGA	1140
GATAAAGTTT ATCGAGGATT TTTCTCACT AGTAATAAAT TGTGGGAGGA GTGGCTCTTT	1200
GCTTATGCCC AACATTTCTA AGTTGGTCAT ATCATTCTTT TGCCGGATGA TGCCAAATGC	1260
ACTCGCCAGG CTCTCTTCTA GCTTTCGAGA GTGTTGCTA GATTCATTTG TGTACTCACT	1320

TGAGCCCTTT AATTTTCCG TTAATTTAGT GGATATAACT CCTGATTTCT TTGAGCATTT	1380
ATTTCTCTTC TCCTGCCTAA ATGAGTTGAT CGAGGAGGAC GTTGAAGAGG TCATGGACAA	1440
TTCTTGGTTT GGACTTGGGG ACTTACAATT CAATCGCCAG AGGGCCCCGT TCTTTCTTGG	1500
GTCTTCATAT TGGCTCAACT CCAAATTTTC AGTTGAGCAC AAGTTTTCAG GCACCATCAA	1560
TTCTCAAATC ATGCAAGTTA TTTTATCTTT GATCCCATTT TCTGATGATC CCACTTTTAG	1620
GCCATCTTCT ACAGAGGTTA ACCTTGCACT ATCAGAGGTT AAGGCTGCGC TAGAAGCTAC	1680
TGGGCAGTCA AAATTGTTCA GGTTTTTGGT GGACGACTGT GCTATGCGTG AGGTTAGAAG	1740
TTCCTATAAG GTGGGCCTTT TTAAGCACAT AAAAGCCCTC ACTCATTGCT TTAATTCTTG	1800
TGGCCTCCAA TGGTTCTCC TTAGGCAAAG GTCCAACCTC AAATTTCTGA AGGACAGGGC	1860
ATCGTCCTTT GCTGATCTTG ATTGTGAGGT TATCAAAGTT TATCAGCTTG TAACATCACA	1920
GGCAATACTT CCTGAGGCTC TGCTTAGCTT GACCAAAGTC TTTGTCAGGG ATTCTGACTC	1980
AAAGGGTGTT TCCATTCCCA GATTGGTCTC GAGAAATGAG CTAGAGGAAC TAGCTCACCC	2040
AGCTAATTCA GCCCTTGAGG AGCCTCAATC AGTTGATTGT AATGCAGGCA GGGTTCAAGC	2100
AAGCGTTTCA AGTTCCCAGC AGCTTGCCGA CACCCACTCT CTTGGTAGCG TTAAGTCATC	2160
AATTGAGACA GCTAACAAGG CTTTTAACTT GGAGGAGCTA AGGATCATGA TTAGAGTCTT	2220
GCCGGAGGAT TTAACTGGG TGGCGAAGAA CATTGGTTTT AAAGACAGGC TGAGAGGCAG	2280
GGGTGCATCA TTCTTCTCAA AACCAGGAAT TTCATGTCAT AGTTACAATG GTGGGAGCCA	2340
CACAAGCTTA GGGTGGCCAA AGTTCATGGA TCAGATTCTA AGCTCCACTG GTGGACGTAA	2400
TTACTACAAT TCATGCCTGG CTCAGATCTA TGAGGAAAAT TCAAAATTGG CTCTTCATAA	2460
GGATGATGAG AGTTGCTATG AAATTGGGCA CAAAGTTTTG ACTGTTAATT TAATCGGCTC	2520
AGCAACTTTC ACTATTAGTA AGTCGCGAAA TTTGGTTGGG GGTAAATCATT GCAGCCTGAC	2580
AATTGGGCCA AATGAGTTTT TCGAAATGCC TAGGGGCATG CAATGCAATT ACTTCCATGG	2640
GGTTTCCAAT TGTACGCCAG GCGGGGTATC GCTGACCTTT AGGCGCCAAA AGTTGGAAGA	2700
TGATGATTTG ATCTTCATAA ATCCACAGGT GCCCATGAG CTCAATCATG AAAAGCTTGA	2760
CCGAAGTATG TGGCAGATGG GCCTTCATGG AATTAAGAAA TCTATTTCTA TGAATGGCAC	2820
GAGTTTTACC TCAGACCTAT GCTCTGTTT CTCTTGCCAC AACTTTCATA AATTCAAGGA	2880
TCTCATCAAT AACTTGAGAT TGGCCCTAGG AGCACAAGGG CTAGGTCAGT GTGACAGGGT	2940
TGTGTTTGCA ACAACAGGTC CTGGTCTATC TAAGGTTTTA GAAATGCCTC GGAGCAAAAA	3000
GCAATCAATT TTGGTTCTTG AAGGTGCCCT ATCCATAGAA ACAGATTATG GTCCAAAAGT	3060
CCTGGGGTCT TTTGAAGTTT TCAAAGGGGA CTTTCACATT AAGAAGATGG AGGAAGGTTC	3120

AATTTTGTGTA ATAACGTACA AGGCCCCAAT TAGATCCACT GGCAGGTTGA GGGTTCACAG	3180
TTCAGAATGC TCATTTTCCG GATCCAAAGA GGTATTGCTA GGCTGCCAGA TTGAGGCATG	3240
TGCTGATTAT GATATTGATG ATTTTAACAC TTTCTCTGTG CCTGGTGATG GCAATTGCTT	3300
TTGGCATTCT GTTGGTTTTT TACTTAGCAC TGATGGACTT GCCCTAAAGG CCGGTATTCG	3360
ATCTTTCGTG GAGAGTGAGC GCTTGGAAG TCCAGATCTT TCAGCCCCAG CAATTTCTAA	3420
ACAATTGGAA GAGAATGCTT ATGCCGAGAA TGAGATGATC GCATTATTCT GCATTCGGCA	3480
CCACGTAAGG CCTATAGTGA TCACACCAGA ATATGAAGTT AGTTGGAAAT TCGGGGAAGG	3540
TGAGTGGCCC CTATGTGGAA TTCTTTCCT TAAATCAAAT CACTTCCAAC CATGCGCCCC	3600
ACTGAATGGT TGCATGATCA CAGCCATTGC TTCAGCACTT GGAAGGCGTG AAGTTGATGT	3660
GTTAAATTAT CTGTGTAGAC CCAGCACTAA TCATATTTTT GAGGAGCTTT GTCAGGGAGG	3720
GGGCCTTAAC ATGATGTATT TAGCTGAAGC TTTTGAGGCC TTTGACATTT GCGCTAAATG	3780
TGATATAAAT GGAGAGATTG AAGTGATTAA TCCGTGTGGT AAAATTTCTG CATTGTTTGA	3840
CATAACTAAT GAGCACATAA GGCATGTTGA GAAAATAGGT AATGGCCCTC AGAGCATAAA	3900
AGTGGATGAA TTGCGGAAGG TCAAGCGATC CGCCCTCGAT TTCCTTTCAA TGAATGGGTC	3960
TAAAATAACC TACTTCCCAA GCTTTGAGCG GGCTGAAAAG TTGCAAGGAT GTTTGCTAGG	4020
GGGCCTAACT GCGGTTATAA GTGATGAGAA GTTCAGTGAT GCAAAACCTT GGCTTTCTGG	4080
TATATCTACT ACTGATATTA AGCCAAGGGA ATTGACTGTC GTGCTTGGTA CATTTGGGGC	4140
TGGGAAGAGT TTCTTGACAA AGAGTTTCAT GAAAAGGTCT GAGGGTAAAT TCGTAACCTT	4200
TGTTTCTCCC AGACGTGCTT TAGCAAATTC AATCAAAAAT GATCTTGAAA TGGATGATAG	4260
CTGCAAAGTT GCTAAAGCAG GTAGGTCAAA GAAGGAAGGG TGGGATGTAG TAACTTTTGA	4320
GGTTTTCTCT AGAAAAGTTG CAGGATTGAA GGCTGGCCAC TGTGTGATTT TTGATGAGGT	4380
CCAGTTGTTT CCTCCTGGAT ACATCGATCT ATGCTTGCTT ATTATACGTA GTGATGCTTT	4440
CATTTCACTT GCTGGTGATC CATGTCAAAG CACATATGAC TCGCAAAGG ATCGGGCAAT	4500
TTTGGGCGCT GAGCAGAGTG ACATACTTAG ACTGCTTGAG GGCAAAACGT ATAGGTATAA	4560
CATAGAAAGC AGGAGGTTTG TGAACCCAAT GTTCGAATCA AGACTGCCAT GTCATTCAA	4620
AAAGGGCTCG ATGACTGCCG CTTTCGCTGA TTATGCAATC TTCCATAATA TGCATGACTT	4680
TCTCCTGGCG AGGTCAAAG GTCCCTTGGA TGCCGTTTTG GTTTCCAGTT TTGAGGAGAA	4740
AAAGATAGTC CAGTCCTACT TTGGAATGAA ACAGCTCACA CTCACATTTG GTGAATCAAC	4800
TGGGTTGAAT TTCAAAAATG GGGGAATTCT CATATCACAT GATTCCTTTC ACACAGATGA	4860
TCGGCGGTGG CTTACTGCTT TATCTCGCTT CAGCCACAAT TTGGATTTGG TGAACATCAC	4920

AGGTCTGAGG GTGGAAAGTT TTCTCTCGCA CTTTGCTGGC AAACCCCTCT ACCATTTTTT	4980
AACAGCCAAA AGTGGGGAGA ATGTCATACG AGATTGCTC CCAGGTGAGC CTAATTCTT	5040
CAGTGGCTTT AACGTTAGCA TTGGAAAGAA TGAAGGTGTT AGGGAGGAGA AGTTATGTGG	5100
TGACCCATGG TTAAAAGTTA TGCTTTTCCT GGGTCAAGAT GAGGATTGTG AAGTTGAAGA	5160
GATGGAGTCA GAATGCTCAA ATGAAGAATG GTTTAAAACC CACATCCCCT TGAGTAATCT	5220
GGAGTCAACC AGGGCCAGGT GGGTGGGTAA AATGGCCTTG AAAGAGTATC GGGAGGTGCG	5280
TTGTGGTTAT GAAATGACTC AACAATTCTT TGATGAGCAT AGGGGTGGAA CTGGTGAGCA	5340
ACTGAGCAAT GCATGTGAGA GGTGTGAAAG CATTTACCCA AGGCATAAAG GAAATGATTC	5400
AATAACCTTC CTCATGGCTG TCCGAAAGCG TCTCAAATTT TCGAAGCCCC AGGTTGAAGC	5460
TGCCAAACTG AGGCGGGCCA AACCATATGG GAAATCTTA TTAGATTCTT TCCTATCCAA	5520
AATCCCATTG AAAGCCAGTC ATAATTCCAT CATGTTTCAT GAAGCGGTAC AGGAGTTTGA	5580
GGCGAAGAAG GCTAGTAAGA GTGCAGCAAC TATAGAGAAT CATGCAGGTA GGTCATGCAG	5640
GGATTGGTTA TTAGATGTTG CTCTGATTTT TATGAAGTCA CAACACTGTA CTAAATTTGA	5700
CAACAGGCTT AGAGTAGCTA AAGCTGGGCA AACCTTGCT TGCTTCCAAC ATGCTGTTCT	5760
GGTTCGCTTT GCACCCTATA TGAGATACAT TGAGAAAAAG CTAATGCAAG CTCTGAAGCC	5820
TAATTCTAC ATCCATTGAG GGAAAGGTCT GACGAGCTGA ACGAGTGGGT CAGAACTAGA	5880
GGATTCACTG GAATTTGCAC AGAATCAGAC TACGAAGCCT TTGATGCTTC CCAAGACCAC	5940
TTCATCCTAG CATTCGAATT GCAGATAATG AAATTTTTGG GGTACCTGA AGATTTAATT	6000
TTGGACTATG AATTCATAAA AATTCATTG GGATCAAAGC TCGGATCATT CTCTATAATG	6060
AGGTTTACTG GGGAGGCCAG CACATTTCTG TTAAACACTA TGGCTAACAT GTTGTTACC	6120
TTTCTGAGGT ACGAACTAAC AGGCTCTGAG TCAATAGCAT TTGCAGGTGA TGACATGTGT	6180
GCTAATCGAA GGTTGCGGCT TAAAACAGAG CATGAGGGTT TTCTGAACAT GATTTGCCTT	6240
AAGGCCAAGG TTCAGTTTGT TTCCAATCCC ACATTCTGCG GATGGTGTTT ATTTAAGGAA	6300
GGGATCTTCA AGAAGCCTCA ATTAATCTGG GAGCGGATAT GCATTGCTAG GGAGATGGGC	6360
AACCTGGAGA ATTGTATTGA CAATTATGCG ATAGAGGTCT CCTATGCATA CCGACTGGGA	6420
GAGCTAGCCA TTGAAATGAT GACCGAGGAA GAAGTGGAGG CCCATTATAA TTGTGTTAGA	6480
TTCTTGGTCA GGAACAAGCA TAAGATGAGA TGCTCAATTT CAGGCCTATT TGAAGCTATT	6540
GATTAGGCCT TAAGTATTTG GCATTATTTG AGTATTATGA ATAATTTAGT TAAAGCATTG	6600
TCAGCATTTG AGTTTGTAGG TGTTTTCAGT GTGCTTAAAT TTCCAGTAGT CATTATAGT	6660
GTGCCTGGTA GTGGTAAAAG TAGTTTAATA AGGGAGCTAA TTTCCGAGGA TGAGAATTTT	6720

ATAGCTTTCA CAGCAGGTGT TCCAGACAGC CCTAATCTCA CAGGAAGGTA CATTAAGCCT	6780
TATTCTCCAG GGTGTGCAGT GCCAGGGAAA GTTAATATAC TTGATGAGTA CTTGTCCGTC	6840
CAAGATTTTT CAGGTTTTGA TGTGCTGTTT TCGGACCCAT ACCAAAACAT CAGCATTCCT	6900
AAAGAGGCAC ATTTTCATCA GTCAAAACT TGTAGGTTTG GCGTGAATAC TTGCAAATAT	6960
CTTTCCTCCT TCGGTTTTAA GGTAGCAGT GACGGTTTGG ACAAAGTCAT TGTGGGGTCG	7020
CCTTTTACAC TAGATGTTGA AGGGGTGCTA ATATGCTTTG GTAAGGAGGC AGTGGATCTC	7080
GCTGTTGCGC ACAACTCTGA ATTCAAATTA CTTGTGAAG TTAGAGGTTC AACTTTTAAC	7140
GTCGTAATC TTTTGAAATC AAGAGATCCA ACCCCAGAGG ATAGGCACTG GTTTTACATT	7200
GCTGCTACAA GACACAGGGA GAAATTGATA ATCATGCAGT AAGATGCCTT TTCAGCAGCC	7260
TGCGAATTGG GCAAAAACCA TAACTCCATT GACAGTTGGC TTGGGCATTG GGCTTGTGCT	7320
GCATTTTCTG AGGAAGTCAA ATCTACCTTA TTCAGGGGAC AACATCCATC AATTCCCTCA	7380
CGGTGGGCGT TACAGGGACG GTACAAAAG TATAACTTAC TGTGGTCCAA AGCAATCCTT	7440
CCCCAGCTCT GGGATATTCG GCCAATCTGA GAATTTTGTG CCCTTAATGC TTGTCATAGG	7500
TCTAATCGCA TTCATACATG TATTGTCTGT TTGGAATTCT GGTCTTGGTA GGAATTGTAA	7560
TTGCCATCCA AATCCTTGCT CATGTAGACA GCAGTAGTGG CAACCACCAA GGTGCTTCA	7620
TTAGGGCCAC TGGAGAGTCA ATTTTGATTG AAAACTGCGG CCCAAGTGAG GCCCTTGCAT	7680
CCACTGTGAA GGAGGTGCTG GGAGGTTTGA AGGCTTTAGG GGTTAGCCGT GCTGTTGAAG	7740
AAATTGATTA TCATTGTTAA ATTGGCTGAA TGGCAAGTCA AATTGGGAAA CTCCCCGGTG	7800
AATCAAATGA GGCTTTTGAA GCCCGGCTAA AATCGCTGGA GTTAGCTAGA GCTCAAAAGC	7860
AGCCGGAAGG TTCTAATGCA CCACCTACTC TCAGTGGCAT TCTTGCCAAA CGCAAGAGGA	7920
TTATAGAGAA TGCACTTTCA AAGACGGTGG ACATGAGGGA GGTTTTGAAA CACGAAACGG	7980
TGGTGATTTT CCCAAATGTC ATGGATGAAG GTGCAATAGA CGAGCTGATT CGTGCATTTG	8040
GTGAATCTGG CATAGCTGAA AGCGTGCAAT TTGATGTGGC CATAGATATA GCACGTCCT	8100
GCTCTGATGT TGGTAGCTCC CAGAGGTCAA CCCTGATTGG CAAGAGTCCA TTTTGTGACC	8160
TAAACAGATC AGAAATAGCT GGGATTATAA GGGAGGTGAC CACATTACGT AGATTTTGCA	8220
TGTACTATGC AAAAATCGTG TGGAACATCC ATCTGGAGAC GGGGATACCA CCAGCTAACT	8280
GGGCCAAGAA AGGATTTAAT GAGAATGAAA AGTTTGCAGC CTTTGATTTT TTCTTGGGAG	8340
TCACAGATGA GAGTGCCTT GAACCAAAGG GTGGAATTAA AAGAGCTCCA ACGAAAGCTG	8400
AGATGGTTGC TAATATCGCC TCTTTTGAGG TTCAAGTGCT CAGACAAGCT ATGGCTGAAG	8460
GCAAGCGGAG TTCCAACCTT GGAGAGATTA GTGGTGAAC GGCTGGTGCA CTCATCAACA	8520

ACCCCTTTTC AAATGTTACA CATGAATGAG GATGACGAAG TCAGCGACAA TTCCGCAGTC	8580
CAATAATTCC CCGATTTCAA GGCTGGGTTA AGCCTGTTTCG CTGGAATACC GTACTAATAG	8640
TATTCCCTTT CCATGCTAAA TCCTATTTAA TATATAAGGT GTGGAAAGTA AAAGAAGATT	8700
TGGTGTGTTT TTATAGTTTT CATTCAAAAA AAAAAAAAAA AAA	8743

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCCCTCT CTTATAGGCC TGCTGTTGAA GAGGTGCTCG CAAAATTCAC CTCTGATGAA	60
CAATCCAGGG TTTCTGCTAC AGCTCTCAAG GCATTAGTAG ACTTAGAGGA AAGTCAGCAC	120
AATTTGTTCT CTTTCGCATT GCCTGATAGA AGCAAAGAAA GGCTGATATC TTCTGGCATT	180
TACTTAAGTC CTTACAGTTT CAGACCCAC TCACATCCAG TTTGTAAAC TTTAGAAAAT	240
CACATTTTGT ACAATGTTTT ACCTAGTTAT GTTAATAATT CATTTTACTT TGTAGGAATC	300
AAGGATTTTA AGCTGCAGTT CTTGAAAAGG AGGAATAAGG ATCTCAGCTT GGTAGCACTC	360
ATAAATAGGT TTGTGACAAG TCGTGATGTT AGTAGGTATG GGTCTGAGTT CGTTATAAGT	420
TCTAGTGACA AATCAAGTCA GGTTGTCAGT AGAAAGGGCA TTGGTGATTC TAACACACTC	480
CGGAGATTGG TCCCACGTGT AATTTCCACA GGTGCCAGGA ATCTTTTCT GCATGATGAG	540
ATTCACTACT GGTCAATTAG TGATCTGATC AATTTTTTGG ACGTTGCCAA GCCAAGCATG	600
CTCTTGCGAA CTGCAGTAAT CCCTCCAGAA GTGCTGGTTG GCTCTCCAGA GAGTCTTAAC	660
CCTTGGGCCT ACCAGTATAA AATCAATGGC AACCAACTGC TCTTCGCACC AGATGGCAAC	720
TGGAATGAGA TGTAATCACA ACCTTTGTCA TGCAGATACC TGCTCAAGGC CAGATCTGTA	780
GTTCTGCCCC ATGGCTCAGC CTACTCGGTT GACATCATTC ACTCAAATT TAGTCACCAC	840
TTGCTTAGTT TCACCCCTAT GGGTAATCTT TTGACTTCAA ACATGCGATG TTTTCTGGC	900
TTCGATGCAA TAGGCATAAA AGATCTTGAA CCTCTAAGCC GCGGCATGCA CAGTTGCTTC	960
CCAGTACATC ATGATGTTGT AACTAAGATA TATCTTTATT TGAGAACTCT CAAGAAGCCA	1020
GATAAGGAGT CTGCCGAGGC AAAGCTTCGA CAACTCATAG AAAAACCAC AGGGAGGGAG	1080
ATAAAGTTTA TCGAGGATTT TTCCTACTA GTAATAAATT GTGGGAGGAG TGGCTCTTTG	1140

CTTATGCCCA ACATTTCTAA GTTGGTCATA TCATTCTTTT GCCGGATGAT GCCAAATGCA	1200
CTCGCCAGGC TCTCTTCTAG CTTTCGAGAG TGTTTCGCTAG ATTCATTTGT GTACTCACTT	1260
GAGCCCTTTA ATTTTCCGT TAATTTAGTG GATATAACTC CTGATTTCTT TGAGCATTTA	1320
TTTCTCTTCT CCTGCCTAAA TGAGTTGATC GAGGAGGACG TTGAAGAGGT CATGGACAAT	1380
TCTTGGTTTG GACTTGGGGA CTTACAATTC AATCGCCAGA GGGCCCCGTT CTTTCTTGGG	1440
TCTTCATATT GGCTCAACTC CAAATTTTCA GTTGAGCACA AGTTTTCAGG CACCATCAAT	1500
TCTCAAATCA TGCAAGTTAT TTTATCTTTG ATCCCATTTT CTGATGATCC CACTTTTAGG	1560
CCATCTTCTA CAGAGGTAA CCTTGCACTA TCAGAGGTTA AGGCTGCGCT AGAAGCTACT	1620
GGGCAGTCAA AATTGTTTCTAG GTTTTTGGTG GACGACTGTG CTATGCGTGA GGTTAGAAGT	1680
TCCTATAAGG TGGGCCTTTT TAAGCACATA AAAGCCCTCA CTCATTGCTT TAATTCTTGT	1740
GGCCTCCAAT GGTTCCTCCT TAGGCAAAGG TCCAACCTCA AATTTCTGAA GGACAGGGCA	1800
TCGTCCTTTG CTGATCTTGA TTGTGAGGTT ATCAAAGTTT ATCAGCTTGT AACATCACAG	1860
GCAATACTTC CTGAGGCTCT GCTTAGCTTG ACCAAAGTCT TTGTCAGGGA TTCTGACTCA	1920
AAGGGTGTTT CCATTCCCAG ATTGGTCTCG AGAAATGAGC TAGAGGAACT AGCTCACCCA	1980
GCTAATTCAG CCCTTGAGGA GCCTCAATCA GTTGATTGTA ATGCAGGCAG GGTTCAAGCA	2040
AGCGTTTCAA GTTCCCAGCA GCTTGCCGAC ACCCACTCTC TTGGTAGCGT TAAGTCATCA	2100
ATTGAGACAG CTAACAAGGC TTTTAACTTG GAGGAGCTAA GGATCATGAT TAGAGTCTTG	2160
CCGGAGGATT TTAAGTGGGT GGCGAAGAAC ATTGGTTTTA AAGACAGGCT GAGAGGCAGG	2220
GGTGCATCAT TCTTCTCAA ACCAGGAATT TCATGTCATA GTTACAATGG TGGGAGCCAC	2280
ACAAGCTTAG GGTGGCCAAA GTTCATGGAT CAGATTCTAA GCTCCACTGG TGGACGTAAT	2340
TACTACAATT CATGCCTGGC TCAGATCTAT GAGGAAAATT CAAAATTGGC TCTTCATAAG	2400
GATGATGAGA GTTGCTATGA AATTGGGCAC AAAGTTTTGA CTGTTAATTT AATCGGCTCA	2460
GCAACTTTCA CTATTAGTAA GTCGCGAAAT TTGGTTGGGG GTAATCATTG CAGCCTGACA	2520
ATTGGGCCAA ATGAGTTTTT CGAAATGCCT AGGGGCATGC AATGCAATTA CTTCCATGGG	2580
GTTTCCAATT GTACGCCAGG GCGGGTATCG CTGACCTTTA GGCGCCAAAA GTTGGAAGAT	2640
GATGATTTGA TCTTCATAAA TCCACAGGTG CCCATTGAGC TCAATCATGA AAAGCTTGAC	2700
CGAAGTATGT GGCAGATGGG CCTTCATGGA ATTAAGAAAT CTATTTCTAT GAATGGCACG	2760
AGTTTTACCT CAGACCTATG CTCTTGTTTC TCTTGCCACA ACTTTCATAA ATTCAAGGAT	2820
CTCATCAATA ACTTGAGATT GGCCCTAGGA GCACAAGGGC TAGGTCAGTG TGACAGGGTT	2880
GTGTTTGCAA CAACAGGTCC TGGTCTATCT AAGGTTTTAG AAATGCCTCG GAGCAAAAAG	2940

CAATCAATTT TGGTTCTTGA AGGTGCCCTA TCCATAGAAA CAGATTATGG TCCAAAAGTC	3000
CTGGGGTCTT TTGAAGTTTT CAAAGGGGAC TTTCACATTA AGAAGATGGA GGAAGGTTCA	3060
ATTTTTGTAA TAACGTACAA GGCCCCAATT AGATCCACTG GCAGGTTGAG GGTTCACAGT	3120
TCAGAATGCT CATTTTCCGG ATCCAAAGAG GTATTGCTAG GCTGCCAGAT TGAGGCATGT	3180
GCTGATTATG ATATTGATGA TTTTAACACT TTCTCTGTGC CTGGTGATGG CAATTGCTTT	3240
TGGCATTCTG TTGGTTTTTT ACTTAGCACT GATGGACTTG CCCTAAAGGC CGGTATTCGA	3300
TCTTTCGTGG AGAGTGAGCG CTTGGTAAGT CCAGATCTTT CAGCCCCAGC AATTTCTAAA	3360
CAATTGGAAG AGAATGCTTA TGCCGAGAAT GAGATGATCG CATTATTCTG CATTCGGCAC	3420
CACGTAAGGC CTATAGTGAT CACACCAGAA TATGAAGTTA GTTGGAAATT CGGGGAAGGT	3480
GAGTGGCCCC TATGTGGAAT TCTTTGCCTT AAATCAAATC ACTTCCAACC ATGCGCCCCA	3540
CTGAATGGTT GCATGATCAC AGCCATTGCT TCAGCACTTG GAAGGCGTGA AGTTGATGTG	3600
TTAAATTATC TGTGTAGACC CAGCACTAAT CATATTTTTG AGGAGCTTTG TCAGGGAGGG	3660
GGCCTTAACA TGATGTATTT AGCTGAAGCT TTTGAGGCCT TTGACATTTG CGCTAAATGT	3720
GATATAAATG GAGAGATTGA AGTGATTAAT CCGTGTGGTA AAATTTCTGC ATTGTTTGAC	3780
ATAACTAATG AGCACATAAG GCATGTTGAG AAAATAGGTA ATGGCCCTCA GAGCATAAAA	3840
GTGGATGAAT TGCGGAAGGT CAAGCGATCC GCCCTCGATT TCCTTTCAAT GAATGGGTCT	3900
AAAATAACCT ACTTCCCAAG CTTTGAGCGG GCTGAAAAGT TGCAAGGATG TTTGCTAGGG	3960
GGCCTAACTG GCGTTATAAG TGATGAGAAG TTCAGTGATG CAAAACCTTG GCTTTCTGGT	4020
ATATCTACTA CTGATATTAA GCCAAGGGAA TTGACTGTCTG TGCTTGGTAC ATTTGGGGCT	4080
GGGAAGAGTT TCTTGTACAA GAGTTTCATG AAAAGGTCTG AGGGTAAATT CGTAACCTTT	4140
GTTTCTCCCA GACGTGCTTT AGCAAATTCA ATCAAAAATG ATCTTGAAAT GGATGATAGC	4200
TGCAAAGTTG CTAAAGCAGG TAGGTCAAAG AAGGAAGGGT GGGATGTAGT AACTTTTGAG	4260
GTTTTCCTTA GAAAAGTTGC AGGATTGAAG GCTGGCCACT GTGTGATTTT TGATGAGGTC	4320
CAGTTGTTTC CTCCTGGATA CATCGATCTA TGCTTGCTTA TTATACGTAG TGATGCTTTC	4380
ATTTCACTTG CTGGTGATCC ATGTCAAAGC ACATATGACT CGCAAAGGA TCGGGCAATT	4440
TTGGGCGCTG AGCAGAGTGA CATACTTAGA CTGCTTGAGG GCAAACGTA TAGGTATAAC	4500
ATAGAAAGCA GGAGGTTTGT GAACCCAATG TTCGAATCAA GACTGCCATG TCACTTCAAA	4560
AAGGGCTCGA TGAAGTCCGC TTTCGCTGAT TATGCAATCT TCCATAATAT GCATGACTTT	4620
CTCCTGGCGA GGTCAAAAGG TCCCTTGGAT GCCGTTTTGG TTTCCAGTTT TGAGGAGAAA	4680
AAGATAGTCC AGTCCTACTT TGGAATGAAA CAGCTCACAC TCACATTTGG TGAATCAACT	4740

GGGTTGAATT TCAAAAATGG GGAATTCTC ATATCACATG ATTCCTTTCA CACAGATGAT	4800
CGGCGGTGGC TTACTGCTTT ATCTCGCTTC AGCCACAATT TGGATTGGT GAACATCACA	4860
GGTCTGAGGG TGGAAAGTTT TCTCTCGCAC TTTGCTGGCA AACCCCTCTA CCATTTTTTA	4920
ACAGCCAAAA GTGGGGAGAA TGTCATACGA GATTTGCTCC CAGGTGAGCC TAACTTCTTC	4980
AGTGGCTTTA ACGTTAGCAT TGGAAAGAAT GAAGGTGTTA GGGAGGAGAA GTTATGTGGT	5040
GACCCATGGT TAAAAGTTAT GCTTTTCTG GGTCAAGATG AGGATTGTGA AGTTGAAGAG	5100
ATGGAGTCAG AATGCTCAAA TGAAGAATGG TTTAAAACCC ACATCCCCTT GAGTAATCTG	5160
GAGTCAACCA GGGCCAGGTG GGTGGGTAAA ATGGCCTTGA AAGAGTATCG GGAGGTGCGT	5220
TGTGGTTATG AAATGACTCA ACAATTCTTT GATGAGCATA GGGGTGGAAC TGGTGAGCAA	5280
CTGAGCAATG CATGTGAGAG GTTTGAAAGC ATTTACCCAA GGCATAAAGG AAATGATTCA	5340
ATAACCTTCC TCATGGCTGT CCGAAAGCGT CTCAAATTTT CGAAGCCCCA GGTTGAAGCT	5400
GCCAACTGA GGCGGGCCAA ACCATATGGG AAATCTTAT TAGATTCTTT CCTATCCAAA	5460
ATCCCATGA AAGCCAGTCA TAATTCCATC ATGTTTCATG AAGCGGTACA GGAGTTTGAG	5520
GCGAAGAAGG CTAGTAAGAG TGCAGCAACT ATAGAGAATC ATGCAGGTAG GTCATGCAGG	5580
GATTGGTTAT TAGATGTTGC TCTGATTTTT ATGAAGTCAC AACACTGTAC TAAATTTGAC	5640
AACAGGCTTA GAGTAGCTAA AGCTGGGCAA ACCCTTGCTT GCTTCCAACA TGCTGTTCTG	5700
GTTGCTTTG CACCCATATG GAGATACATT GAGAAAAAGC TAATGCAAGC TCTGAAGCCT	5760
AACTTCTACA TCCATTCAGG GAAAGGTCTG ACGAGCTGAA CGAGTGGGTC AGAACTAGAG	5820
GATTCACTGG AATTGACACA GAATCAGACT ACGAAGCCTT TGATGCTTCC CAAGACCACT	5880
TCATCCTAGC ATTCGAATTG CAGATAATGA AATTTTGGG GTTACCTGAA GATTTAATTT	5940
TGGACTATGA ATTCATAAAA ATTCATTTGG GATCAAAGCT CGGATCATTC TCTATAATGA	6000
GGTTTACTGG GGAGGCCAGC ACATTTCTGT TTAACACTAT GGCTAACATG TTGTTACCT	6060
TTCTGAGGTA CGAACTAACA GGCTCTGAGT CAATAGCATT TGCAGGTGAT GACATGTGTG	6120
CTAATCGAAG GTTGCGGCTT AAAACAGAGC ATGAGGGTTT TCTGAACATG ATTTGCCTTA	6180
AGGCCAAGGT TCAGTTTGTT TCCAATCCCA CATTCTGCGG ATGGTGTTTA TTTAAGGAAG	6240
GGATCTTCAA GAAGCCTCAA TTAATCTGGG AGCGGATATG CATTGCTAGG GAGATGGGCA	6300
ACCTGGAGAA TTGTATTGAC AATTATGCGA TAGAGGTCTC CTATGCATAC CGACTGGGAG	6360
AGCTAGCCAT TGAAATGATG ACCGAGGAAG AAGTGGAGGC CCATTATAAT TGTGTTAGAT	6420
TCTTGCTCAG GAACAAGCAT AAGATGAGAT GCTCAATTTT AGGCCTATTT GAAGCTATTG	6480
ATTAG	6485

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Leu	Ser	Tyr	Arg	Pro	Ala	Val	Glu	Glu	Val	Leu	Ala	Lys	Phe
1				5					10					15	
Thr	Ser	Asp	Glu	Gln	Ser	Arg	Val	Ser	Ala	Thr	Ala	Leu	Lys	Ala	Leu
			20					25					30		
Val	Asp	Leu	Glu	Glu	Ser	Gln	His	Asn	Leu	Phe	Ser	Phe	Ala	Leu	Pro
		35					40					45			
Asp	Arg	Ser	Lys	Glu	Arg	Leu	Ile	Ser	Ser	Gly	Ile	Tyr	Leu	Ser	Pro
		50				55					60				
Tyr	Ser	Phe	Arg	Pro	His	Ser	His	Pro	Val	Cys	Lys	Thr	Leu	Glu	Asn
65					70					75					80
His	Ile	Leu	Tyr	Asn	Val	Leu	Pro	Ser	Tyr	Val	Asn	Asn	Ser	Phe	Tyr
				85					90					95	
Phe	Val	Gly	Ile	Lys	Asp	Phe	Lys	Leu	Gln	Phe	Leu	Lys	Arg	Arg	Asn
			100					105					110		
Lys	Asp	Leu	Ser	Leu	Val	Ala	Leu	Ile	Asn	Arg	Phe	Val	Thr	Ser	Arg
		115					120						125		
Asp	Val	Ser	Arg	Tyr	Gly	Ser	Glu	Phe	Val	Ile	Ser	Ser	Ser	Asp	Lys
		130				135					140				
Ser	Ser	Gln	Val	Val	Ser	Arg	Lys	Gly	Ile	Gly	Asp	Ser	Asn	Thr	Leu
145					150					155					160
Arg	Arg	Leu	Val	Pro	Arg	Val	Ile	Ser	Thr	Gly	Ala	Arg	Asn	Leu	Phe
				165					170					175	
Leu	His	Asp	Glu	Ile	His	Tyr	Trp	Ser	Ile	Ser	Asp	Leu	Ile	Asn	Phe
			180					185					190		
Leu	Asp	Val	Ala	Lys	Pro	Ser	Met	Leu	Leu	Ala	Thr	Ala	Val	Ile	Pro
		195					200					205			
Pro	Glu	Val	Leu	Val	Gly	Ser	Pro	Glu	Ser	Leu	Asn	Pro	Trp	Ala	Tyr
		210				215					220				
Gln	Tyr	Lys	Ile	Asn	Gly	Asn	Gln	Leu	Leu	Phe	Ala	Pro	Asp	Gly	Asn
225					230					235					240

Trp	Asn	Glu	Met	Tyr	Ser	Gln	Pro	Leu	Ser	Cys	Arg	Tyr	Leu	Leu	Lys	245	250	255
Ala	Arg	Ser	Val	Val	Leu	Pro	Asp	Gly	Ser	Arg	Tyr	Ser	Val	Asp	Ile	260	265	270
Ile	His	Ser	Lys	Phe	Ser	His	His	Leu	Leu	Ser	Phe	Thr	Pro	Met	Gly	275	280	285
Asn	Leu	Leu	Thr	Ser	Asn	Met	Arg	Cys	Phe	Ser	Gly	Phe	Asp	Ala	Ile	290	295	300
Gly	Ile	Lys	Asp	Leu	Glu	Pro	Leu	Ser	Arg	Gly	Met	His	Ser	Cys	Phe	305	310	315
Pro	Val	His	His	Asp	Val	Val	Thr	Lys	Ile	Tyr	Leu	Tyr	Leu	Arg	Thr	325	330	335
Leu	Lys	Lys	Pro	Asp	Lys	Glu	Ser	Ala	Glu	Ala	Lys	Leu	Arg	Gln	Leu	340	345	350
Ile	Glu	Lys	Pro	Thr	Gly	Arg	Glu	Ile	Lys	Phe	Ile	Glu	Asp	Phe	Ser	355	360	365
Ser	Leu	Val	Ile	Asn	Cys	Gly	Arg	Ser	Gly	Ser	Leu	Leu	Met	Pro	Asn	370	375	380
Ile	Ser	Lys	Leu	Val	Ile	Ser	Phe	Phe	Cys	Arg	Met	Met	Pro	Asn	Ala	385	390	395
Leu	Ala	Arg	Leu	Ser	Ser	Ser	Phe	Arg	Glu	Cys	Ser	Leu	Asp	Ser	Phe	405	410	415
Val	Tyr	Ser	Leu	Glu	Pro	Phe	Asn	Phe	Ser	Val	Asn	Leu	Val	Asp	Ile	420	425	430
Thr	Pro	Asp	Phe	Phe	Glu	His	Leu	Phe	Leu	Phe	Ser	Cys	Leu	Asn	Glu	435	440	445
Leu	Ile	Glu	Glu	Asp	Val	Glu	Glu	Val	Met	Asp	Asn	Ser	Trp	Phe	Gly	450	455	460
Leu	Gly	Asp	Leu	Gln	Phe	Asn	Arg	Gln	Arg	Ala	Pro	Phe	Phe	Leu	Gly	465	470	475
Ser	Ser	Tyr	Trp	Leu	Asn	Ser	Lys	Phe	Ser	Val	Glu	His	Lys	Phe	Ser	485	490	495
Gly	Thr	Ile	Asn	Ser	Gln	Ile	Met	Gln	Val	Ile	Leu	Ser	Leu	Ile	Pro	500	505	510
Phe	Ser	Asp	Asp	Pro	Thr	Phe	Arg	Pro	Ser	Ser	Thr	Glu	Val	Asn	Leu	515	520	525
Ala	Leu	Ser	Glu	Val	Lys	Ala	Ala	Leu	Glu	Ala	Thr	Gly	Gln	Ser	Lys	530	535	540
Leu	Phe	Arg	Phe	Leu	Val	Asp	Asp	Cys	Ala	Met	Arg	Glu	Val	Arg	Ser	545	550	555

Ser Tyr Lys Val Gly Leu Phe Lys His Ile Lys Ala Leu Thr His Cys
565 570 575

Phe Asn Ser Cys Gly Leu Gln Trp Phe Leu Leu Arg Gln Arg Ser Asn
580 585 590

Leu Lys Phe Leu Lys Asp Arg Ala Ser Ser Phe Ala Asp Leu Asp Cys
595 600 605

Glu Val Ile Lys Val Tyr Gln Leu Val Thr Ser Gln Ala Ile Leu Pro
610 615 620

Glu Ala Leu Leu Ser Leu Thr Lys Val Phe Val Arg Asp Ser Asp Ser
625 630 635 640

Lys Gly Val Ser Ile Pro Arg Leu Val Ser Arg Asn Glu Leu Glu Glu
645 650 655

Leu Ala His Pro Ala Asn Ser Ala Leu Glu Glu Pro Gln Ser Val Asp
660 665 670

Cys Asn Ala Gly Arg Val Gln Ala Ser Val Ser Ser Ser Gln Gln Leu
675 680 685

Ala Asp Thr His Ser Leu Gly Ser Val Lys Ser Ser Ile Glu Thr Ala
690 695 700

Asn Lys Ala Phe Asn Leu Glu Glu Leu Arg Ile Met Ile Arg Val Leu
705 710 715 720

Pro Glu Asp Phe Asn Trp Val Ala Lys Asn Ile Gly Phe Lys Asp Arg
725 730 735

Leu Arg Gly Arg Gly Ala Ser Phe Phe Ser Lys Pro Gly Ile Ser Cys
740 745 750

His Ser Tyr Asn Gly Gly Ser His Thr Ser Leu Gly Trp Pro Lys Phe
755 760 765

Met Asp Gln Ile Leu Ser Ser Thr Gly Gly Arg Asn Tyr Tyr Asn Ser
770 775 780

Cys Leu Ala Gln Ile Tyr Glu Glu Asn Ser Lys Leu Ala Leu His Lys
785 790 795 800

Asp Asp Glu Ser Cys Tyr Glu Ile Gly His Lys Val Leu Thr Val Asn
805 810 815

Leu Ile Gly Ser Ala Thr Phe Thr Ile Ser Lys Ser Arg Asn Leu Val
820 825 830

Gly Gly Asn His Cys Ser Leu Thr Ile Gly Pro Asn Glu Phe Phe Glu
835 840 845

Met Pro Arg Gly Met Gln Cys Asn Tyr Phe His Gly Val Ser Asn Cys
850 855 860

Thr Pro Gly Arg Val Ser Leu Thr Phe Arg Arg Gln Lys Leu Glu Asp
865 870 875 880

Asp	Asp	Leu	Ile	Phe	Ile	Asn	Pro	Gln	Val	Pro	Ile	Glu	Leu	Asn	His		
				885					890					895			
Glu	Lys	Leu	Asp	Arg	Ser	Met	Trp	Gln	Met	Gly	Leu	His	Gly	Ile	Lys		
			900					905					910				
Lys	Ser	Ile	Ser	Met	Asn	Gly	Thr	Ser	Phe	Thr	Ser	Asp	Leu	Cys	Ser		
		915					920					925					
Cys	Phe	Ser	Cys	His	Asn	Phe	His	Lys	Phe	Lys	Asp	Leu	Ile	Asn	Asn		
	930					935					940						
Leu	Arg	Leu	Ala	Leu	Gly	Ala	Gln	Gly	Leu	Gly	Gln	Cys	Asp	Arg	Val		
945					950					955					960		
Val	Phe	Ala	Thr	Thr	Gly	Pro	Gly	Leu	Ser	Lys	Val	Leu	Glu	Met	Pro		
				965					970					975			
Arg	Ser	Lys	Lys	Gln	Ser	Ile	Leu	Val	Leu	Glu	Gly	Ala	Leu	Ser	Ile		
			980					985					990				
Glu	Thr	Asp	Tyr	Gly	Pro	Lys	Val	Leu	Gly	Ser	Phe	Glu	Val	Phe	Lys		
		995					1000					1005					
Gly	Asp	Phe	His	Ile	Lys	Lys	Met	Glu	Glu	Gly	Ser	Ile	Phe	Val	Ile		
	1010						1015					1020					
Thr	Tyr	Lys	Ala	Pro	Ile	Arg	Ser	Thr	Gly	Arg	Leu	Arg	Val	His	Ser		
1025					1030					1035					1040		
Ser	Glu	Cys	Ser	Phe	Ser	Gly	Ser	Lys	Glu	Val	Leu	Leu	Gly	Cys	Gln		
				1045					1050					1055			
Ile	Glu	Ala	Cys	Ala	Asp	Tyr	Asp	Ile	Asp	Asp	Phe	Asn	Thr	Phe	Ser		
			1060					1065					1070				
Val	Pro	Gly	Asp	Gly	Asn	Cys	Phe	Trp	His	Ser	Val	Gly	Phe	Leu	Leu		
		1075					1080					1085					
Ser	Thr	Asp	Gly	Leu	Ala	Leu	Lys	Ala	Gly	Ile	Arg	Ser	Phe	Val	Glu		
	1090					1095					1100						
Ser	Glu	Arg	Leu	Val	Ser	Pro	Asp	Leu	Ser	Ala	Pro	Ala	Ile	Ser	Lys		
1105					1110					1115					1120		
Gln	Leu	Glu	Glu	Asn	Ala	Tyr	Ala	Glu	Asn	Glu	Met	Ile	Ala	Leu	Phe		
				1125					1130					1135			
Cys	Ile	Arg	His	His	Val	Arg	Pro	Ile	Val	Ile	Thr	Pro	Glu	Tyr	Glu		
			1140					1145					1150				
Val	Ser	Trp	Lys	Phe	Gly	Glu	Gly	Glu	Trp	Pro	Leu	Cys	Gly	Ile	Leu		
		1155					1160					1165					
Cys	Leu	Lys	Ser	Asn	His	Phe	Gln	Pro	Cys	Ala	Pro	Leu	Asn	Gly	Cys		
	1170					1175					1180						
Met	Ile	Thr	Ala	Ile	Ala	Ser	Ala	Leu	Gly	Arg	Arg	Glu	Val	Asp	Val		
1185					1190					1195					1200		

Leu Asn Tyr Leu Cys Arg Pro Ser Thr Asn His Ile Phe Glu Glu Leu
 1205 1210 1215
 Cys Gln Gly Gly Gly Leu Asn Met Met Tyr Leu Ala Glu Ala Phe Glu
 1220 1225 1230
 Ala Phe Asp Ile Cys Ala Lys Cys Asp Ile Asn Gly Glu Ile Glu Val
 1235 1240 1245
 Ile Asn Pro Cys Gly Lys Ile Ser Ala Leu Phe Asp Ile Thr Asn Glu
 1250 1255 1260
 His Ile Arg His Val Glu Lys Ile Gly Asn Gly Pro Gln Ser Ile Lys
 1265 1270 1275 1280
 Val Asp Glu Leu Arg Lys Val Lys Arg Ser Ala Leu Asp Phe Leu Ser
 1285 1290 1295
 Met Asn Gly Ser Lys Ile Thr Tyr Phe Pro Ser Phe Glu Arg Ala Glu
 1300 1305 1310
 Lys Leu Gln Gly Cys Leu Leu Gly Gly Leu Thr Gly Val Ile Ser Asp
 1315 1320 1325
 Glu Lys Phe Ser Asp Ala Lys Pro Trp Leu Ser Gly Ile Ser Thr Thr
 1330 1335 1340
 Asp Ile Lys Pro Arg Glu Leu Thr Val Val Leu Gly Thr Phe Gly Ala
 1345 1350 1355 1360
 Gly Lys Ser Phe Leu Tyr Lys Ser Phe Met Lys Arg Ser Glu Gly Lys
 1365 1370 1375
 Phe Val Thr Phe Val Ser Pro Arg Arg Ala Leu Ala Asn Ser Ile Lys
 1380 1385 1390
 Asn Asp Leu Glu Met Asp Asp Ser Cys Lys Val Ala Lys Ala Gly Arg
 1395 1400 1405
 Ser Lys Lys Glu Gly Trp Asp Val Val Thr Phe Glu Val Phe Leu Arg
 1410 1415 1420
 Lys Val Ala Gly Leu Lys Ala Gly His Cys Val Ile Phe Asp Glu Val
 1425 1430 1435 1440
 Gln Leu Phe Pro Pro Gly Tyr Ile Asp Leu Cys Leu Leu Ile Ile Arg
 1445 1450 1455
 Ser Asp Ala Phe Ile Ser Leu Ala Gly Asp Pro Cys Gln Ser Thr Tyr
 1460 1465 1470
 Asp Ser Gln Lys Asp Arg Ala Ile Leu Gly Ala Glu Gln Ser Asp Ile
 1475 1480 1485
 Leu Arg Leu Leu Glu Gly Lys Thr Tyr Arg Tyr Asn Ile Glu Ser Arg
 1490 1495 1500
 Arg Phe Val Asn Pro Met Phe Glu Ser Arg Leu Pro Cys His Phe Lys
 1505 1510 1515 1520

Lys Gly Ser Met Thr Ala Ala Phe Ala Asp Tyr Ala Ile Phe His Asn
1525 1530 1535

Met His Asp Phe Leu Leu Ala Arg Ser Lys Gly Pro Leu Asp Ala Val
1540 1545 1550

Leu Val Ser Ser Phe Glu Glu Lys Lys Ile Val Gln Ser Tyr Phe Gly
1555 1560 1565

Met Lys Gln Leu Thr Leu Thr Phe Gly Glu Ser Thr Gly Leu Asn Phe
1570 1575 1580

Lys Asn Gly Gly Ile Leu Ile Ser His Asp Ser Phe His Thr Asp Asp
1585 1590 1595 1600

Arg Arg Trp Leu Thr Ala Leu Ser Arg Phe Ser His Asn Leu Asp Leu
1605 1610 1615

Val Asn Ile Thr Gly Leu Arg Val Glu Ser Phe Leu Ser His Phe Ala
1620 1625 1630

Gly Lys Pro Leu Tyr His Phe Leu Thr Ala Lys Ser Gly Glu Asn Val
1635 1640 1645

Ile Arg Asp Leu Leu Pro Gly Glu Pro Asn Phe Phe Ser Gly Phe Asn
1650 1655 1660

Val Ser Ile Gly Lys Asn Glu Gly Val Arg Glu Glu Lys Leu Cys Gly
1665 1670 1675 1680

Asp Pro Trp Leu Lys Val Met Leu Phe Leu Gly Gln Asp Glu Asp Cys
1685 1690 1695

Glu Val Glu Glu Met Glu Ser Glu Cys Ser Asn Glu Glu Trp Phe Lys
1700 1705 1710

Thr His Ile Pro Leu Ser Asn Leu Glu Ser Thr Arg Ala Arg Trp Val
1715 1720 1725

Gly Lys Met Ala Leu Lys Glu Tyr Arg Glu Val Arg Cys Gly Tyr Glu
1730 1735 1740

Met Thr Gln Gln Phe Phe Asp Glu His Arg Gly Gly Thr Gly Glu Gln
1745 1750 1755 1760

Leu Ser Asn Ala Cys Glu Arg Phe Glu Ser Ile Tyr Pro Arg His Lys
1765 1770 1775

Gly Asn Asp Ser Ile Thr Phe Leu Met Ala Val Arg Lys Arg Leu Lys
1780 1785 1790

Phe Ser Lys Pro Gln Val Glu Ala Ala Lys Leu Arg Arg Ala Lys Pro
1795 1800 1805

Tyr Gly Lys Phe Leu Leu Asp Ser Phe Leu Ser Lys Ile Pro Leu Lys
1810 1815 1820

Ala Ser His Asn Ser Ile Met Phe His Glu Ala Val Gln Glu Phe Glu
1825 1830 1835 1840

Ala Lys Lys Ala Ser Lys Ser Ala Ala Thr Ile Glu Asn His Ala Gly
1845 1850 1855

Arg Ser Cys Arg Asp Trp Leu Leu Asp Val Ala Leu Ile Phe Met Lys
1860 1865 1870

Ser Gln His Cys Thr Lys Phe Asp Asn Arg Leu Arg Val Ala Lys Ala
1875 1880 1885

Gly Gln Thr Leu Ala Cys Phe Gln His Ala Val Leu Val Arg Phe Ala
1890 1895 1900

Pro Tyr Met Arg Tyr Ile Glu Lys Lys Leu Met Gln Ala Leu Lys Pro
1905 1910 1915 1920

Asn Phe Tyr Ile His Ser Gly Lys Gly Leu Asp Glu Leu Asn Glu Trp
1925 1930 1935

Val Arg Thr Arg Gly Phe Thr Gly Ile Cys Thr Glu Ser Asp Tyr Glu
1940 1945 1950

Ala Phe Asp Ala Ser Gln Asp His Phe Ile Leu Ala Phe Glu Leu Gln
1955 1960 1965

Ile Met Lys Phe Leu Gly Leu Pro Glu Asp Leu Ile Leu Asp Tyr Glu
1970 1975 1980

Phe Ile Lys Ile His Leu Gly Ser Lys Leu Gly Ser Phe Ser Ile Met
1985 1990 1995 2000

Arg Phe Thr Gly Glu Ala Ser Thr Phe Leu Phe Asn Thr Met Ala Asn
2005 2010 2015

Met Leu Phe Thr Phe Leu Arg Tyr Glu Leu Thr Gly Ser Glu Ser Ile
2020 2025 2030

Ala Phe Ala Gly Asp Asp Met Cys Ala Asn Arg Arg Leu Arg Leu Lys
2035 2040 2045

Thr Glu His Glu Gly Phe Leu Asn Met Ile Cys Leu Lys Ala Lys Val
2050 2055 2060

Gln Phe Val Ser Asn Pro Thr Phe Cys Gly Trp Cys Leu Phe Lys Glu
2065 2070 2075 2080

Gly Ile Phe Lys Lys Pro Gln Leu Ile Trp Glu Arg Ile Cys Ile Ala
2085 2090 2095

Arg Glu Met Gly Asn Leu Glu Asn Cys Ile Asp Asn Tyr Ala Ile Glu
2100 2105 2110

Val Ser Tyr Ala Tyr Arg Leu Gly Glu Leu Ala Ile Glu Met Met Thr
2115 2120 2125

Glu Glu Glu Val Glu Ala His Tyr Asn Cys Val Arg Phe Leu Val Arg
2130 2135 2140

Asn Lys His Lys Met Arg Cys Ser Ile Ser Gly Leu Phe Glu Ala Ile
2145 2150 2155 2160

Asp

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAATAATT TAGTTAAAGC ATTGTCAGCA TTTGAGTTTG TAGGTGTTTT CAGTGTGCTT	60
AAATTTCCAG TAGTCATTCA TAGTGTGCCT GGTAGTGGTA AAAGTAGTTT AATAAGGGAG	120
CTAATTTCCG AGGATGAGAA TTTCATAGCT TTCACAGCAG GTGTTCCAGA CAGCCCTAAT	180
CTCACAGGAA GGTACATTAA GCCTTATTCT CCAGGGTGTG CAGTGCCAGG GAAAGTTAAT	240
ATACTTGATG AGTACTTGTC CGTCCAAGAT TTTTCAGGTT TTGATGTGCT GTTCTCGGAC	300
CCATACCAAA ACATCAGCAT TCCTAAAGAG GCACATTTCA TCAAGTCAAA AACTTGTAGG	360
TTTGGCGTGA ATACTTGCAA ATATCTTTCC TCCTTCGGTT TTAAGGTTAG CAGTGACGGT	420
TTGGACAAAG TCATTGTGGG GTCGCCTTTT AACTAGATG TTGAAGGGGT GCTAATATGC	480
TTTGGTAAGG AGGCAGTGGA TCTCGCTGTT GCGCACAACT CTGAATTCAA ATTACCTTGT	540
GAAGTTAGAG GTTCAACTTT TAACGTCGTA ACTCTTTTGA AATCAAGAGA TCCAACCCCA	600
GAGGATAGGC ACTGGTTTTA CATTGCTGCT ACAAGACACA GGGAGAAATT GATAATCATG	660
CAG	663

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 221 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Asn	Asn	Leu	Val	Lys	Ala	Leu	Ser	Ala	Phe	Glu	Phe	Val	Gly	Val
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCCTTTTC	AGCAGCCTGC	GAATTGGGCA	AAAACCATAA	CTCCATTGAC	AGTTGGCTTG	60
GGCATTGGGC	TTGTGCTGCA	TTTTCTGAGG	AAGTCAAATC	TACCTTATTC	AGGGGACAAC	120
ATCCATCAAT	TCCCTCACGG	TGGGCGTTAC	AGGGACGGTA	CAAAAAGTAT	AACTTACTGT	180

GGTCCAAAGC AATCCTTCCC CAGCTCTGGG ATATTCGGCC AATCTGAGAA TTTTGTGCCC 240
 TTAATGCTTG TCATAGGTCT AATCGCATTC ATACATGTAT TGTCTGTTTG GAATTCTGGT 300
 CTTGGTAGGA ATTGTAATTG CCATCCAAAT CCTTGCTCAT GTAGACAGCA G 351

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Pro	Phe	Gln	Gln	Pro	Ala	Asn	Trp	Ala	Lys	Thr	Ile	Thr	Pro	Leu
1				5					10					15	
Thr	Val	Gly	Leu	Gly	Ile	Gly	Leu	Val	Leu	His	Phe	Leu	Arg	Lys	Ser
			20					25					30		
Asn	Leu	Pro	Tyr	Ser	Gly	Asp	Asn	Ile	His	Gln	Phe	Pro	His	Gly	Gly
			35				40					45			
Arg	Tyr	Arg	Asp	Gly	Thr	Lys	Ser	Ile	Thr	Tyr	Cys	Gly	Pro	Lys	Gln
	50					55					60				
Ser	Phe	Pro	Ser	Ser	Gly	Ile	Phe	Gly	Gln	Ser	Glu	Asn	Phe	Val	Pro
65					70				75					80	
Leu	Met	Leu	Val	Ile	Gly	Leu	Ile	Ala	Phe	Ile	His	Val	Leu	Ser	Val
				85				90						95	
Trp	Asn	Ser	Gly	Leu	Gly	Arg	Asn	Cys	Asn	Cys	His	Pro	Asn	Pro	Cys
			100				105						110		
Ser	Cys	Arg	Gln	Gln											
			115												

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGTATTGTC TGT TTGGAAT TCTGGTCTTG GTAGGAATTG TAATTGCCAT CCAAATCCTT	60
GCTCATGTAG ACAGCAGTAG TGGCAACCAC CAAGGTTGCT TCATTAGGGC CACTGGAGAG	120
TCAATTTTGA TTGAAACTG CGGCCCAAGT GAGGCCCTTG CATCCACTGT GAAGGAGGTG	180
CTGGGAGGTT TGAAGGCTTT AGGGGTTAGC CGTGCTGTTG AAGAAATTGA TTATCATTGT	240

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Tyr	Cys	Leu	Phe	Gly	Ile	Leu	Val	Leu	Val	Gly	Ile	Val	Ile	Ala
1				5					10					15	
Ile	Gln	Ile	Leu	Ala	His	Val	Asp	Ser	Ser	Ser	Gly	Asn	His	Gln	Gly
			20					25					30		
Cys	Phe	Ile	Arg	Ala	Thr	Gly	Glu	Ser	Ile	Leu	Ile	Glu	Asn	Cys	Gly
		35					40					45			
Pro	Ser	Glu	Ala	Leu	Ala	Ser	Thr	Val	Lys	Glu	Val	Leu	Gly	Gly	Leu
	50					55					60				
Lys	Ala	Leu	Gly	Val	Ser	Arg	Ala	Val	Glu	Glu	Ile	Asp	Tyr	His	Cys
65					70					75					80

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGGCAAGTC AAATTGGGAA ACTCCCCGGT GAATCAAATG AGGCTTTTGA AGCCCGGCTA	60
AAATCGCTGG AGTTAGCTAG AGCTCAAAG CAGCCGGAAG GTTCTAATGC ACCACCTACT	120

```

CTCAGTGGCA TTCTTGCCAA ACGCAAGAGG ATTATAGAGA ATGCACTTTC AAAGACGGTG      180
GACATGAGGG AGGTTTTGAA ACACGAAACG GTGGTGATTT CCCCAAATGT CATGGATGAA      240
GGTGCAATAG ACGAGCTGAT TCGTGCAATT GGTGAATCTG GCATAGCTGA AAGCGTGCAA      300
TTTGATGTGG CCATAGATAT AGCACGTCAC TGCTCTGATG TTGGTAGCTC CCAGAGTTCA      360
ACCCTGATTG GCAAGAGTCC ATTTTGTGAC CTAAACAGAT CAGAAATAGC TGGGATTATA      420
AGGGAGGTGA CCACATTACG TAGATTTTGC ATGTACTATG CAAAAATCGT GTGGAACATC      480
CATCTGGAGA CGGGGATACC ACCAGCTAAC TGGGCCAAGA AAGGATTTAA TGAGAATGAA      540
AAGTTTGCAG CCTTTGATTT TTTCTTGGA GTCACAGATG AGAGTGCCT TGAACCAAAG      600
GGTGGAATTA AAAGAGCTCC AACGAAAGCT GAGATGGTTG CTAATATCGC CTCTTTTGAG      660
GTTCAAGTGC TCAGACAAGC TATGGCTGAA GGCAAGCGGA GTTCCAACCT TGGAGAGATT      720
AGTGGTGGAA CGGCTGGTGC ACTCATCAAC AACCCTTTT CAAATGTTAC ACATGAA      777

```

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Ala Ser Gln Ile Gly Lys Leu Pro Gly Glu Ser Asn Glu Ala Phe
 1             5             10             15

Glu Ala Arg Leu Lys Ser Leu Glu Leu Ala Arg Ala Gln Lys Gln Pro
 20             25             30

Glu Gly Ser Asn Ala Pro Pro Thr Leu Ser Gly Ile Leu Ala Lys Arg
 35             40             45

Lys Arg Ile Ile Glu Asn Ala Leu Ser Lys Thr Val Asp Met Arg Glu
 50             55             60

Val Leu Lys His Glu Thr Val Val Ile Ser Pro Asn Val Met Asp Glu
 65             70             75             80

Gly Ala Ile Asp Glu Leu Ile Arg Ala Phe Gly Glu Ser Gly Ile Ala
 85             90             95

Glu Ser Val Gln Phe Asp Val Ala Ile Asp Ile Ala Arg His Cys Ser
100             105             110

Asp Val Gly Ser Ser Gln Ser Ser Thr Leu Ile Gly Lys Ser Pro Phe
115             120             125

```

Cys	Asp	Leu	Asn	Arg	Ser	Glu	Ile	Ala	Gly	Ile	Ile	Arg	Glu	Val	Thr
130						135					140				
Thr	Leu	Arg	Arg	Phe	Cys	Met	Tyr	Tyr	Ala	Lys	Ile	Val	Trp	Asn	Ile
145					150					155					160
His	Leu	Glu	Thr	Gly	Ile	Pro	Pro	Ala	Asn	Trp	Ala	Lys	Lys	Gly	Phe
				165					170					175	
Asn	Glu	Asn	Glu	Lys	Phe	Ala	Ala	Phe	Asp	Phe	Phe	Leu	Gly	Val	Thr
			180					185					190		
Asp	Glu	Ser	Ala	Leu	Glu	Pro	Lys	Gly	Gly	Ile	Lys	Arg	Ala	Pro	Thr
		195					200					205			
Lys	Ala	Glu	Met	Val	Ala	Asn	Ile	Ala	Ser	Phe	Glu	Val	Gln	Val	Leu
	210					215					220				
Arg	Gln	Ala	Met	Ala	Glu	Gly	Lys	Arg	Ser	Ser	Asn	Leu	Gly	Glu	Ile
225					230					235					240
Ser	Gly	Gly	Thr	Ala	Gly	Ala	Leu	Ile	Asn	Asn	Pro	Phe	Ser	Asn	Val
				245					250					255	
Thr	His	Glu													

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCTGGGCAA ACTTTGGCCT GCTTTCAACA CGCCGTCTTG GTTCGCTTTG CACCCTACAT	60
GCGATACATT GAAAAGAAGC TTGTGCAGGC ATTGAAACCA AATTTCTACA TTCATTCTGG	120
CAAAGGTCTT GATGAGCTAA GTGAATGGGT TAGAGCCAGA GGTTCACAG GTGTGTGTAC	180
TGAGTCAGAC TATGAAGCTT TTGATGCATC CCAAGATCAT TTCATCCTGG CATTGAACT	240
GCAAATCATG AGATTTT TAGACTGCCAGA AGATCTGATT TTAGATTATG AGTTCATCAA	300
AATTCATCTT GGGTCAAAGC TTGGCTCTTT TGCAATTATG AGATTCACAG GTGAGGCAAG	360
CACCTTCCTA TTCAATACTA TGGCCAACAT GCTATTCACT TTCCTGAGGT ATGAGTTGAC	420
AGGTTCTGAA TCAATTGCAT TTGCTGGAGA TGATATGTGT GCTAATCGCA GGTAAAGACT	480
CAAGACTGAG CACGCCGGCT TTCTAAACAT GATCTGTCTC AAAGCTAAGG TGCAGTTTGT	540

CACAAATCCC ACCTTCTGTG GATGGTGTTT GTTTAAAGAG GGAATCTTTA AAAAACCCCA	600
GCTCATTTGG GAAAGGATCT GCATTGCTAG GGAAATGGGT AACTTGGACA ATTGCATTGA	660
CAATTACGCA ATTGAGGTGT CTTATGCTTA CAGACTTGGG GAATTGTCCA TAGGCGTGAT	720
GACTGAGGAG GAAGTTGAAG CACATTCTAA CTGCGTGCCT TTCCTGGTTC GCAATAAGCA	780
CAAGATGAGG TGCTCAATTT CTGGTTTGTT TGAAGTAATT GTTTAGGCCT TAAGTGTTTG	840
GCATGGTGTG AGTATTATGA ATAACCTAGT CAAAGCTTTG TCTGCTTTTG AATTTGTTGG	900
TGTGTTTTGT GTACTTAAAT TTCCAGTTGT TGTTACAGT GTTCCAGGTA GCGGTAAAAG	960
TAGCCTAATA AGGGAGCTCA TTTCTGAAGA CGAGGCTTTT GTGGCCTTTA CAGCAGGTGT	1020
GCCAGACAGT CCAAATCTGA CAGGGAGGTA CATCAAGCCC TACGCTCCAG GGTGTGCAGT	1080
GCAAGGGAAA ATAAACATAC TTGATGAGTA CTTGTCTGTC TCTGATACTT CTGGCTTTGA	1140
TGTGCTGTTT TCAGACCCTT ACCAGAATGT CAGCATTCCA AGGGAGGCAC ACTTCATAAA	1200
AACCAAAACC TGTAGGTTTG GTACCAACAC CTGCAAGTAC CTTCAATCTT TTGGCTTTAA	1260
TGTTTGTAGT GATGGGGTGG ATAAAGTTGT TGTAGGGTCG CCATTTGAAC TGGAGGTTGA	1320
GGGGGTTCTC ATTTGCTTTG GAAAGGAGGC TGTAGATCTA GCAGTTGCAC ACAATTCTGA	1380
CTTCAAGTTG CCCTGCGAGG TCGGGGGTTC AACATTTGAC GTTGTAACGT TATTGAAGTC	1440
CAGGGATCCA ACTTCAGAAG ATAAGCATTG GTTCTACGTT GCAGCCACAA GGCATCGAAG	1500
TAAACTGATA ATAATGCAGT AAAATGCCTT TTCAGCAACC TGCCAACTGG GCTAAGACCA	1560
TAACTCCATT AACTATTGGT TTGGGCATTG GGTGTTCTT GCACTTCTTA AGGAAATCAA	1620
ATCTGCCATA TTCAGGAGAC AATATTCACC AGTTCACACA CGGAGGGCAT TACAGGGACG	1680
GCACGAAGAG TATAACCTAT TGTGGCCCTA GGCAGTCATT CCAAGCTCA GGAATATTCG	1740
GTCAGTCTGA AAATTTCTGA CCTCTAATAT TGGTCGTGAC TCTGGTCTGCT TTTATACATG	1800
CGTTATCTCT TTGGAATTCT GGTCTAGTA GGAGTTGCAA TTGCCATCCA AATCCTTGCA	1860
CATGTAGACA GCAGTAGTGG CAACCATCAA GGCTGTTTCA TAAGAGCCAC CGGGGAGTCA	1920
ATAGTAATTG AGAATTGTGG GCCGAGCGAG GCCCTAGCTG CTACAGTCAA AGAGGTGTTG	1980
GGCGGTCTAA AGGCTTTAGG GGTTAGCCAA AAGGTTGATG AAATTAATTA CAGTTGTTGA	2040
GACAGTTGAA TGGCAAGTCA AGTTGGAAAA TTGCCTGGCG AATCAAATGA AGCATATGAG	2100
GCTAGACTCA AGGCTTTAGA GTTAGCAAGG GCCCAAAAAG CTCCAGAAGT CTCCAACCAA	2160
CCTCCACAC TTGGAGGCAT TCTAGCCAAA AGGAAAAGAG TGATTGAGAA TGCACCTCTCA	2220
AAGACAGTGG ATATGCGTGA AGTCTTAAGG CATGAATCTG TTGTACTCTC CCCGAATGTA	2280
ATGGACGAGG GAGCAATAGA CGAGCTGATT CGTGCCTTTG GGGAGTCGGG CATAGCTGAA	2340

AATGTGCAGT TTGATGTTGC AATAGACATT GCTCGCCACT GTTCTGATGT GGGGAGCTCT	2400
CAGAGGTCAA CCCTTATTGG TAAAAGCCCC TTCTGTGAGT TAAATAGGTC TGAAATTGCC	2460
GGAATAATAA GGGAGGTGAC CACGCTGCGC AGATTTTGCA TGTACTACGC AAAGATTGTG	2520
TGGAACATCC ATTTGGAGAC GGGAATACCA CCAGCTAATT GGGCCAAGAA AGGATTTAAT	2580
GAGAATGAAA AGTTTGCAGC CTTTGA CTTC TTCCTTGGAG TCACAGATGA AAGCGCGCTT	2640
GAGCCTAAGG GTGGAGTCAA GAGAGCTCCA ACAAAGCAG	2680

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 767 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGCGATACA TTGAAAAGAA GCTTGTGCAG GCATTGAAAC CAAATTTCTA CATTCAATTCT	60
GGCAAAGGTC TTGATGAGCT AAGTGAATGG GTTAGAGCCA GAGGTTTCAC AGGTGTGTGT	120
ACTGAGTCAG ACTATGAAGC TTTTGATGCA TCCCAAGATC ATTTTCATCCT GGCATTTGAA	180
CTGCAAATCA TGAGATTTTT AGGACTGCCA GAAGATCTGA TTTTAGATTA TGAGTTCATC	240
AAAATTCATC TTGGGTCAAA GCTTGGCTCT TTTGCAATTA TGAGATTCAC AGGTGAGGCA	300
AGCACCTTCC TATTCAATAC TATGGCCAAC ATGCTATTCA CTTTCCTGAG GTATGAGTTG	360
ACAGGTTCTG AATCAATTGC ATTTGCTGGA GATGATATGT GTGCTAATCG CAGGTTAAGA	420
CTCAAGACTG AGCACGCCGG CTTTCTAAAC ATGATCTGTC TCAAAGCTAA GGTGCAGTTT	480
GTCACAAATC CCACCTTCTG TGGATGGTGT TTGTTTAAAG AGGGAATCTT TAAAAAACCC	540
CAGCTCATTT GGGAAAGGAT CTGCATTGCT AGGGAATGG GTAACCTGGA CAATTGCATT	600
GACAATTACG CAATTGAGGT GTCTTATGCT TACAGACTTG GGAATTGTC CATAGGCGTG	660
ATGACTGAGG AGGAAGTTGA AGCACATTCT AACTGCGTGC GTTTCCTGGT TCGCAATAAG	720
CACAAGATGA GGTGCTCAAT TTCTGGTTTG TTTGAAGTAA TTGTTTA	767

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Arg	Tyr	Ile	Glu	Lys	Lys	Leu	Val	Gln	Ala	Leu	Lys	Pro	Asn	Phe	
1				5					10					15		
Tyr	Ile	His	Ser	Gly	Lys	Gly	Leu	Asp	Glu	Leu	Ser	Glu	Trp	Val	Arg	
			20					25					30			
Ala	Arg	Gly	Phe	Thr	Gly	Val	Cys	Thr	Glu	Ser	Asp	Tyr	Glu	Ala	Phe	
		35					40					45				
Asp	Ala	Ser	Gln	Asp	His	Phe	Ile	Leu	Ala	Phe	Glu	Leu	Gln	Ile	Met	
	50					55					60					
Arg	Phe	Leu	Gly	Leu	Pro	Glu	Asp	Leu	Ile	Leu	Asp	Tyr	Glu	Phe	Ile	
65					70					75					80	
Lys	Ile	His	Leu	Gly	Ser	Lys	Leu	Gly	Ser	Phe	Ala	Ile	Met	Arg	Phe	
			85						90					95		
Thr	Gly	Glu	Ala	Ser	Thr	Phe	Leu	Phe	Asn	Thr	Met	Ala	Asn	Met	Leu	
			100						105				110			
Phe	Thr	Phe	Leu	Arg	Tyr	Glu	Leu	Thr	Gly	Ser	Glu	Ser	Ile	Ala	Phe	
		115					120					125				
Ala	Gly	Asp	Asp	Met	Cys	Ala	Asn	Arg	Arg	Leu	Arg	Leu	Lys	Thr	Glu	
	130					135					140					
His	Ala	Gly	Phe	Leu	Asn	Met	Ile	Cys	Leu	Lys	Ala	Lys	Val	Gln	Phe	
145					150					155					160	
Val	Thr	Asn	Pro	Thr	Phe	Cys	Gly	Trp	Cys	Leu	Phe	Lys	Glu	Gly	Ile	
			165						170					175		
Phe	Lys	Lys	Pro	Gln	Leu	Ile	Trp	Glu	Arg	Ile	Cys	Ile	Ala	Arg	Glu	
			180					185					190			
Met	Gly	Asn	Leu	Asp	Asn	Cys	Ile	Asp	Asn	Tyr	Ala	Ile	Glu	Val	Ser	
		195					200					205				
Tyr	Ala	Tyr	Arg	Leu	Gly	Glu	Leu	Ser	Ile	Gly	Val	Met	Thr	Glu	Glu	
	210					215					220					
Glu	Val	Glu	Ala	His	Ser	Asn	Cys	Val	Arg	Phe	Leu	Val	Arg	Asn	Lys	
225					230					235					240	
His	Lys	Met	Arg	Cys	Ser	Ile	Ser	Gly	Leu	Phe	Glu	Val	Ile	Val		
				245					250					255		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGAATAACT TAGTCAAAGC TTTGTCTGCT TTTGAATTTG TTGGTGTGTT TTGTGTACTT	60
AAATTTCCAG TTGTTGTTCA CAGTGTTCCA GGTAGCGGTA AAAGTAGCCT AATAAGGGAG	120
CTCATTTCTG AAGACGAGGC TTTTGTGGCC TTTACAGCAG GTGTGCCAGA CAGTCCAAAT	180
CTGACAGGGA GGTACATCAA GCCCTACGCT CCAGGGTGTG CAGTGCAAGG GAAAATAAAC	240
ATACTTGATG AGTACTTGTC TGTCTCTGAT ACTTCTGGCT TTGATGTGCT GTTCTCAGAC	300
CCTTACCAGA ATGTCAGCAT TCCAAGGGAG GCACACTTCA TAAAAACCAA AACCTGTAGG	360
TTTGGTACCA ACACCTGCAA GTACCTTCAA TCTTTTGGCT TTAATGTTTG TAGTGATGGG	420
GTGGATAAAG TTGTTGTAGG GTCGCCATTT GAACTGGAGG TTGAGGGGGT TCTCATTTGC	480
TTTGGAAAGG AGGCTGTAGA TCTAGCAGTT GCACACAATT CTGACTTCAA GTTGCCCTGC	540
GAGGTGCGGG GTTCAACATT TGACGTTGTA ACGTTATTGA AGTCCAGGGA TCCAACCTTCA	600
GAAGATAAGC ATTGGTTCTA CGTTGCAGCC ACAAGGCATC GAAGTAACT GATAATAATG	660
CAGTAA	666

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Asn Asn Leu Val Lys Ala Leu Ser Ala Phe Glu Phe Val Gly Val	
1 5 10 15	
Phe Cys Val Leu Lys Phe Pro Val Val Val His Ser Val Pro Gly Ser	
20 25 30	
Gly Lys Ser Ser Leu Ile Arg Glu Leu Ile Ser Glu Asp Glu Ala Phe	
35 40 45	

Val	Ala	Phe	Thr	Ala	Gly	Val	Pro	Asp	Ser	Pro	Asn	Leu	Thr	Gly	Arg				
50						55					60								
Tyr	Ile	Lys	Pro	Tyr	Ala	Pro	Gly	Cys	Ala	Val	Gln	Gly	Lys	Ile	Asn				
65					70					75					80				
Ile	Leu	Asp	Glu	Tyr	Leu	Ser	Val	Ser	Asp	Thr	Ser	Gly	Phe	Asp	Val				
				85					90					95					
Leu	Phe	Ser	Asp	Pro	Tyr	Gln	Asn	Val	Ser	Ile	Pro	Arg	Glu	Ala	His				
			100					105					110						
Phe	Ile	Lys	Thr	Lys	Thr	Cys	Arg	Phe	Gly	Thr	Asn	Thr	Cys	Lys	Tyr				
		115					120					125							
Leu	Gln	Ser	Phe	Gly	Phe	Asn	Val	Cys	Ser	Asp	Gly	Val	Asp	Lys	Val				
	130					135					140								
Val	Val	Gly	Ser	Pro	Phe	Glu	Leu	Glu	Val	Glu	Gly	Val	Leu	Ile	Cys				
145					150					155					160				
Phe	Gly	Lys	Glu	Ala	Val	Asp	Leu	Ala	Val	Ala	His	Asn	Ser	Asp	Phe				
				165					170					175					
Lys	Leu	Pro	Cys	Glu	Val	Arg	Gly	Ser	Thr	Phe	Asp	Val	Val	Thr	Leu				
			180					185					190						
Leu	Lys	Ser	Arg	Asp	Pro	Thr	Ser	Glu	Asp	Lys	His	Trp	Phe	Tyr	Val				
		195					200					205							
Ala	Ala	Thr	Arg	His	Arg	Ser	Lys	Leu	Ile	Ile	Met	Gln							
	210					215					220								

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGCCTTTTC AGCAACCTGC CAACTGGGCT AAGACCATAA CTCCATTAAC TATTGGTTTG	60
GGCATTGGGT TGGTTCTGCA CTTCTTAAGG AAATCAAATC TGCCATATTC AGGAGACAAT	120
ATTCACCACT TCCCACACGG AGGGCATTAC AGGGACGGCA CGAAGAGTAT AACCTATTGT	180
GGCCCTAGGC AGTCATTCCC AAGCTCAGGA ATATTCGGTC AGTCTGAAAA TTTCGTACCT	240
CTAATATTGG TCGTGACTCT GGTGCTTTT ATACATGCGT TATCTCTTTG GAATTCTGGT	300
CCTAGTAGGA GTTGCAATTG CCATCCAAAT CCTTGCACAT GTAGACAGCA GTAG	354

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Pro	Phe	Gln	Gln	Pro	Ala	Asn	Trp	Ala	Lys	Thr	Ile	Thr	Pro	Leu
1				5					10					15	
Thr	Ile	Gly	Leu	Gly	Ile	Gly	Leu	Val	Leu	His	Phe	Leu	Arg	Lys	Ser
		20					25						30		
Asn	Leu	Pro	Tyr	Ser	Gly	Asp	Asn	Ile	His	Gln	Phe	Pro	His	Gly	Gly
		35				40						45			
His	Tyr	Arg	Asp	Gly	Thr	Lys	Ser	Ile	Thr	Tyr	Cys	Gly	Pro	Arg	Gln
	50					55					60				
Ser	Phe	Pro	Ser	Ser	Gly	Ile	Phe	Gly	Gln	Ser	Glu	Asn	Phe	Val	Pro
65					70					75					80
Leu	Ile	Leu	Val	Val	Thr	Leu	Val	Ala	Phe	Ile	His	Ala	Leu	Ser	Leu
			85						90					95	
Trp	Asn	Ser	Gly	Pro	Ser	Arg	Ser	Cys	Asn	Cys	His	Pro	Asn	Pro	Cys
			100					105					110		
Thr	Cys	Arg	Gln	Gln											
			115												

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATGCGTTATC	TCTTTGGAAT	TCTGGTCCTA	GTAGGAGTTG	CAATTGCCAT	CCAAATCCTT	60
GCACATGTAG	ACAGCAGTAG	TGGCAACCAT	CAAGGCTGTT	TCATAAGAGC	CACCGGGGAG	120
TCAATAGTAA	TTGAGAATTG	TGGGCCGAGC	GAGGCCCTAG	CTGCTACAGT	CAAAGAGGTG	180

TTGGGCGGTC TAAAGGCTTT AGGGGTTAGC CAAAAGGTTG ATGAAATTAA TTACAGTTGT 240
TGA 243

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Arg	Tyr	Leu	Phe	Gly	Ile	Leu	Val	Leu	Val	Gly	Val	Ala	Ile	Ala	
1				5					10					15		
Ile	Gln	Ile	Leu	Ala	His	Val	Asp	Ser	Ser	Ser	Gly	Asn	His	Gln	Gly	
			20					25					30			
Cys	Phe	Ile	Arg	Ala	Thr	Gly	Glu	Ser	Ile	Val	Ile	Glu	Asn	Cys	Gly	
			35				40					45				
Pro	Ser	Glu	Ala	Leu	Ala	Ala	Thr	Val	Lys	Glu	Val	Leu	Gly	Gly	Leu	
	50					55					60					
Lys	Ala	Leu	Gly	Val	Ser	Gln	Lys	Val	Asp	Glu	Ile	Asn	Tyr	Ser	Cys	
65						70				75					80	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGGCAAGTC AAGTTGAAA ATGCCTGGC GAATCAAATG AAGCATATGA GGCTAGACTC	60
AAGGCTTTAG AGTTAGCAAG GGCCCAAAA GCTCCAGAAG TCTCCAACCA ACCTCCCACA	120
CTTGAGGCA TTCTAGCCAA AAGGAAAAGA GTGATTGAGA ATGCACTCTC AAAGACAGTG	180
GATATGCGTG AAGTCTTAAG GCATGAATCT GTTGTACTCT CCCCGAATGT AATGGACGAG	240
GGAGCAATAG ACGAGCTGAT TCGTGCCTTT GGGGAGTCGG GCATAGCTGA AAATGTGCAG	300

```

TTTGATGTTG CAATAGACAT TGCTCGCCAC TGTTCGTATG TGGGGAGCTC TCAGAGGTCA      360
ACCCTTATTG GTAAAAGCCC CTTCTGTGAG TTAAATAGGT CTGAAATTGC CGGAATAATA      420
AGGGAGGTGA CCACGCTGCG CAGATTTTGC ATGTACTACG CAAAGATTGT GTGGAACATC      480
CATTGAGAGA CGGGAATACC ACCAGCTAAT TGGGCCAAGA AAGGATTTAA TGAGAATGAA      540
AAGTTTGCAG CCTTTGACTT CTTCTTGGGA GTCACAGATG AAAGCGCGCT TGAGCCTAAG      600
GGTGGAGTCA AGAGAGCTCC AACAAAAGCA G                                     631

```

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Met Ala Ser Gln Val Gly Lys Leu Pro Gly Glu Ser Asn Glu Ala Tyr
1           5           10           15
Glu Ala Arg Leu Lys Ala Leu Glu Leu Ala Arg Ala Gln Lys Ala Pro
20          25          30
Glu Val Ser Asn Gln Pro Pro Thr Leu Gly Gly Ile Leu Ala Lys Arg
35          40          45
Lys Arg Val Ile Glu Asn Ala Leu Ser Lys Thr Val Asp Met Arg Glu
50          55          60
Val Leu Arg His Glu Ser Val Val Leu Ser Pro Asn Val Met Asp Glu
65          70          75          80
Gly Ala Ile Asp Glu Leu Ile Arg Ala Phe Gly Glu Ser Gly Ile Ala
85          90          95
Glu Asn Val Gln Phe Asp Val Ala Ile Asp Ile Ala Arg His Cys Ser
100         105         110
Asp Val Gly Ser Ser Gln Arg Ser Thr Leu Ile Gly Lys Ser Pro Phe
115        120        125
Cys Glu Leu Asn Arg Ser Glu Ile Ala Gly Ile Ile Arg Glu Val Thr
130        135        140
Thr Leu Arg Arg Phe Cys Met Tyr Tyr Ala Lys Ile Val Trp Asn Ile
145        150        155        160
His Leu Glu Thr Gly Ile Pro Pro Ala Asn Trp Ala Lys Lys Gly Phe
165        170        175

```

Asn Glu Asn Glu Lys Phe Ala Ala Phe Asp Phe Phe Leu Gly Val Thr
180 185 190
Asp Glu Ser Ala Leu Glu Pro Lys Gly Gly Val Lys Arg Ala Pro Thr
195 200 205
Lys Ala
210

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2009 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAAGCTAGCA CATTCTGTGTT CAACACTATG GCTAACATGT TGTTCACTTT TCTGAGATAT	60
GAAGTGACGG GTTCAGAGTC AATAGCATTT GCAGGGGATG ATATGTGTGC TAATAGAAGG	120
TTGCGGCTTA AAACGGAGCA TGAGGGTTTT CTGAACATGA TCTGCCTTAA GGCCAAGGTT	180
CAGTTTGTTT CCAACCCAC ATTCTGTGGA TGGTGCTTAT TTAAGGAGGG AATCTTCAAG	240
AAACCTCAAC TAATTTGGGA GCGAATATGC ATAGCCAGAG AGATGGGCAA TCTGGAGAAC	300
TGTATTGACA ATTATGCGAT AGAAGTGTCC TATGCATATA GATTGGGTGA GCTATCAATT	360
GAAATGATGA CAGAAGAAGA AGTGGAGGCA CACTACAATT GTGTGAGGTT CCTGGTTAGG	420
AACAAGCATA AGATGAGGTG CTCAATTTCA GGCCTGTTTG AAGTGTTGA TTAGGCCTTA	480
AGTATTTGGC GTTGTTCGAG TTATTATGAA TAATTTAGTT AAAGCATTAT CAGCCTTCGA	540
GTTTATAGGT GTTTTCAATG TGCTCAAATT TCCAGTTGTT ATACATAGTG TGCCTGGTAG	600
TGGTAAGAGT AGCTTAATAA GGGAATTAAT CTCAGAGGAC GAGAGTTTCG TGGCTTTCAC	660
AGCAGGTGTT CCAGACAGTC CTAACCTCAC AGGGAGGTAC ATCAAGCCTT ACTCACCAGG	720
ATGCGCAGTG CAAGGAAAAG TGAATATACT TGATGAGTAC TTGTCCGTTT AAGACATTTT	780
GGGTTTTGAT GTACTGTTTT CAGACCCGTA CCAGAATATC AGTATTCCCC AAGAGGCGCA	840
TTTCATTAAG TCCAAGACTT GTAGGTTTGG TGTGAACACT TGCAAATACC TTTCTCTTTT	900
CGGTTTCGAA GTTAGCAGCG ACGGGCTGGA CGACGTCATT GTGGGATCGC CCTTCACTCT	960
AGATGTTGAA GGGGTGCTGA TATGTTTTGG CAAGGAGGCG GTAGATCTCG CTGTTGCGCA	1020
CAACTCTGAA TTCAAGTTGC CGTGTGAGGT TCGAGGTTCA ACCTTCAATG TGGTAACCTT	1080

TTTGAAATCA AGAGACCCAA CCCAGAGGA CAGGCACTGG TTTTACATCG CTGCCACAAG	1140
ACATAGGAAG AAATTGGTCA TTATGCAGTA AAATGCCTTT TCAGCAGCCT GCTAATTGGG	1200
CAAAAACCAT AACTCCATTG ACTATTGGCT TAGGAATTGG ACTTGTGCTG CATTTTCTGA	1260
GAAAGTCAAA TCTACCATAT TCAGGAGACA ACATCCATCA ATTCCTCAC GGGGGGCGTT	1320
ACCGGGACGG CACAAAAGT ATAACCTACT GTGGCCCTAA GCAGTCCTTC CCCAGTTCAG	1380
GAATATTTGG TCAGTCTGAG AATTTTGTGC CCTTAATGCT TGTCATAGGT CTAATTGCAT	1440
TCATACATGT ATTGTCTGTT TGGAAATTCTG GTCTTGCTAG GAATTGCAAT TGCCATCCAA	1500
ATCCTTGCTC ATGTAGACAA CAGTAGTGGC AGTCACCAAG GTTGCTTTAT CAGGGCCACT	1560
GGAGAGTCTA TTTTGATTGA AAATTGTGGC CCAAGCGAGG CCCTTGCATC AACAGTGAGG	1620
GAGGTGTTGG GGGGTTTGAA GGCTTTAGGA ATTAGCCATA CTAAGAAGA AATTGATTAT	1680
CGTTGTTAAA TTGGTTAAAT GGCGAGTCAA GTTGGAAGC TCCCGGAGA ATCAAATGAG	1740
GCATTTGAAG CCCGGCTGAA ATCACTGGAG TTGGCTAGAG CTCAAAAGCA GCCAGAAGGT	1800
TCAAACACAC CGCCTACTCT CAGTGGTGTG CTTGCCAAAC GTAAGAGGGT TATTGAGAAT	1860
GCACTCTCAA AGACAGTGGA CATGAGGGAG GTGTTGAAAC ACGAAACGGT TGTAATTTCC	1920
CCAAATGTCA TGGATGAGGG TGCAATAGAT GAACTGATTC GTGCATTTCG AGAATCAGGC	1980
ATAGCTGAGA GCGCACAATT TGATGTGGC	2009

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 447 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAGCTAGCA CATTTCTGTT CAACACTATG GCTAACATGT TGTTCACTTT TCTGAGATAT	60
GAACTGACGG GTTCAGAGTC AATAGCATTT GCAGGGGATG ATATGTGTGC TAATAGAAGG	120
TTGCGGCTTA AAACGGAGCA TGAGGGTTTT CTGAACATGA TCTGCCTTAA GGCCAAGGTT	180
CAGTTTGTTT CCAACCCAC ATTCTGTGGA TGGTGCTTAT TTAAGGAGGG AATCTTCAAG	240
AAACCTCAAC TAATTGGGA GCGAATATGC ATAGCCAGAG AGATGGGCAA TCTGGAGAAC	300
TGTATTGACA ATTATGCGAT AGAAGTGTCC TATGCATATA GATTGGGTGA GCTATCAATT	360
GAAATGATGA CAGAAGAAGA AGTGGAGGCA CACTACAATT GTGTGAGGTT CCTGGTTAGG	420

AACAAGCATA AGATGAGGTG CTCAATT

447

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Glu	Ala	Ser	Thr	Phe	Leu	Phe	Asn	Thr	Met	Ala	Asn	Met	Leu	Phe	Thr	1	5	10	15
Phe	Leu	Arg	Tyr	Glu	Leu	Thr	Gly	Ser	Glu	Ser	Ile	Ala	Phe	Ala	Gly	20	25	30	
Asp	Asp	Met	Cys	Ala	Asn	Arg	Arg	Leu	Arg	Leu	Lys	Thr	Glu	His	Glu	35	40	45	
Gly	Phe	Leu	Asn	Met	Ile	Cys	Leu	Lys	Ala	Lys	Val	Gln	Phe	Val	Ser	50	55	60	
Asn	Pro	Thr	Phe	Cys	Gly	Trp	Cys	Leu	Phe	Lys	Glu	Gly	Ile	Phe	Lys	65	70	75	80
Lys	Pro	Gln	Leu	Ile	Trp	Glu	Arg	Ile	Cys	Ile	Ala	Arg	Glu	Met	Gly	85	90	95	
Asn	Leu	Glu	Asn	Cys	Ile	Asp	Asn	Tyr	Ala	Ile	Glu	Val	Ser	Tyr	Ala	100	105	110	
Tyr	Arg	Leu	Gly	Glu	Leu	Ser	Ile	Glu	Met	Met	Thr	Glu	Glu	Glu	Val	115	120	125	
Glu	Ala	His	Tyr	Asn	Cys	Val	Arg	Phe	Leu	Val	Arg	Asn	Lys	His	Lys	130	135	140	
Met	Arg	Cys	Ser	Ile												145			

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 666 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAATAATT TAGTTAAAGC ATTATCAGCC TTCGAGTTTA TAGGTGTTTT CAATGTGCTC	60
AAATTTCCAG TTGTTATACA TAGTGTGCCT GGTAGTGGTA AGAGTAGCTT AATAAGGGAA	120
TTAATCTCAG AGGACGAGAG TTTCGTGGCT TTCACAGCAG GTGTTCCAGA CAGTCCTAAC	180
CTCACAGGGA GGTACATCAA GCCTTACTCA CCAGGATGCG CAGTGCAAGG AAAAGTGAAT	240
ATACTTGATG AGTACTTGTC CGTTCAAGAC ATTTCCGGGT TTGATGTACT GTTTTCAGAC	300
CCGTACCAGA ATATCAGTAT TCCCCAAGAG GCGCATTTC TTAAGTCCAA GACTTGTAGG	360
TTTGGTGTGA ACACTTGCAA ATACCTTTCC TCTTTCGGTT TCGAAGTTAG CAGCGACGGG	420
CTGGACGACG TCATTGTGGG ATCGCCCTTC ACTCTAGATG TTGAAGGGGT GCTGATATGT	480
TTTGGCAAGG AGGCGGTAGA TCTCGCTGTT GCGCACAACT CTGAATTCAA GTTGCCGTGT	540
GAGGTTTCGAG GTTCAACCTT CAATGTGGTA ACCCTTTTGA AATCAAGAGA CCCAACCCCA	600
GAGGACAGGC ACTGGTTTTA CATCGCTGCC ACAAGACATA GGAAGAAATT GGTCATTATG	660
CAGTAA	666

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Asn Asn Leu Val Lys Ala Leu Ser Ala Phe Glu Phe Ile Gly Val	
1 5 10 15	
Phe Asn Val Leu Lys Phe Pro Val Val Ile His Ser Val Pro Gly Ser	
20 25 30	
Gly Lys Ser Ser Leu Ile Arg Glu Leu Ile Ser Glu Asp Glu Ser Phe	
35 40 45	
Val Ala Phe Thr Ala Gly Val Pro Asp Ser Pro Asn Leu Thr Gly Arg	
50 55 60	
Tyr Ile Lys Pro Tyr Ser Pro Gly Cys Ala Val Gln Gly Lys Val Asn	
65 70 75 80	
Ile Leu Asp Glu Tyr Leu Ser Val Gln Asp Ile Ser Gly Phe Asp Val	
85 90 95	

Leu	Phe	Ser	Asp	Pro	Tyr	Gln	Asn	Ile	Ser	Ile	Pro	Gln	Glu	Ala	His
			100					105					110		
Phe	Ile	Lys	Ser	Lys	Thr	Cys	Arg	Phe	Gly	Val	Asn	Thr	Cys	Lys	Tyr
		115					120					125			
Leu	Ser	Ser	Phe	Gly	Phe	Glu	Val	Ser	Ser	Asp	Gly	Leu	Asp	Asp	Val
	130					135					140				
Ile	Val	Gly	Ser	Pro	Phe	Thr	Leu	Asp	Val	Glu	Gly	Val	Leu	Ile	Cys
145					150					155					160
Phe	Gly	Lys	Glu	Ala	Val	Asp	Leu	Ala	Val	Ala	His	Asn	Ser	Glu	Phe
				165					170					175	
Lys	Leu	Pro	Cys	Glu	Val	Arg	Gly	Ser	Thr	Phe	Asn	Val	Val	Thr	Leu
			180					185					190		
Leu	Lys	Ser	Arg	Asp	Pro	Thr	Pro	Glu	Asp	Arg	His	Trp	Phe	Tyr	Ile
		195					200					205			
Ala	Ala	Thr	Arg	His	Arg	Lys	Lys	Leu	Val	Ile	Met	Gln			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGCCTTTTC AGCAGCCTGC TAATTGGGCA AAAACCATAA CTCCATTGAC TATTGGCTTA	60
GGAATTGGAC TTGTGCTGCA TTTTCTGAGA AAGTCAAATC TACCATATTC AGGAGACAAC	120
ATCCATCAAT TTCCTCACGG GGGGCGTTAC CGGGACGGCA CAAAAGTAT AACTTACTGT	180
GGCCCTAAGC AGTCCTTCCC CAGTTCAGGA ATATTTGGTC AGTCTGAGAA TTTGTGCCC	240
TTAATGCTTG TCATAGGTCT AATTGCATTC ATACATGTAT TGTCTGTTTG GAATTCTGGT	300
CTTGGTAGGA ATTGCAATTG CCATCCAAAT CCTTGCTCAT GTAGACAACA GTAG	354

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Pro	Phe	Gln	Gln	Pro	Ala	Asn	Trp	Ala	Lys	Thr	Ile	Thr	Pro	Leu
1				5					10					15	
Thr	Ile	Gly	Leu	Gly	Ile	Gly	Leu	Val	Leu	His	Phe	Leu	Arg	Lys	Ser
			20					25					30		
Asn	Leu	Pro	Tyr	Ser	Gly	Asp	Asn	Ile	His	Gln	Phe	Pro	His	Gly	Gly
		35					40					45			
Arg	Tyr	Arg	Asp	Gly	Thr	Lys	Ile	Thr	Tyr	Cys	Gly	Pro	Lys	Gln	Ser
	50					55					60				
Phe	Pro	Ser	Ser	Gly	Ile	Phe	Gly	Gln	Ser	Glu	Asn	Phe	Val	Pro	Leu
65					70					75					80
Met	Leu	Val	Ile	Gly	Leu	Ile	Ala	Phe	Ile	His	Val	Leu	Ser	Val	Trp
				85					90					95	
Asn	Ser	Gly	Leu	Gly	Arg	Asn	Cys	Asn	Cys	His	Pro	Asn	Pro	Cys	Ser
			100					105					110		
Cys	Arg	Gln	Gln												
			115												

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGTATTGTC	TGTTTGGAAT	TCTGGTCTTG	GTAGGAATTG	CAATTGCCAT	CCAAATCCTT	60
GCTCATGTAG	ACAACAGTAG	TGGCAGTCAC	CAAGGTTGCT	TTATCAGGGC	CACTGGAGAG	120
TCTATTTTGA	TTGAAAATTG	TGGCCCAAGC	GAGGCCCTTG	CATCAACAGT	GAGGGAGGTG	180
TTGGGGGGTT	TGAAGGCTTT	AGGAATTAGC	CATACTACTG	AAGAAATTGA	TTATCGTTGT	240
TAA						243

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Tyr	Cys	Leu	Phe	Gly	Ile	Leu	Val	Leu	Val	Gly	Ile	Ala	Ile	Ala
1				5				10					15		
Ile	Gln	Ile	Leu	Ala	His	Val	Asp	Asn	Ser	Ser	Gly	Ser	His	Gln	Gly
			20				25						30		
Cys	Phe	Ile	Arg	Ala	Thr	Gly	Glu	Ser	Ile	Leu	Ile	Glu	Asn	Cys	Gly
			35				40					45			
Pro	Ser	Glu	Ala	Leu	Ala	Ser	Thr	Val	Arg	Glu	Val	Leu	Gly	Gly	Leu
			50			55					60				
Lys	Ala	Leu	Gly	Ile	Ser	His	Thr	Thr	Glu	Glu	Ile	Asp	Tyr	Arg	Cys
65				70						75					80

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 311 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGGCGAGTC AAGTTGGTAA GCTCCCCGGA GAATCAAATG AGGCATTGTA AGCCCGGCTG	60
AAATCACTGG AGTTGGCTAG AGCTCAAAAG CAGCCAGAAG GTTCAAACAC ACCGCCTACT	120
CTCAGTGGTG TGCTTGCCAA ACGTAAGAGG GTTATTGAGA ATGCACTCTC AAAGACAGTG	180
GACATGAGGG AGGTGTTGAA ACACGAAACG GTTGTAATTT CCCCAAATGT CATGGATGAG	240
GGTGCAATAG ATGAACTGAT TCGTGCATTC GGAGAATCAG GCATAGCTGA GAGCGCACAA	300
TTTGATGTGG C	311

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met	Ala	Ser	Gln	Val	Gly	Lys	Leu	Pro	Gly	Glu	Ser	Asn	Glu	Ala	Phe	
1				5					10					15		
Glu	Ala	Arg	Leu	Lys	Ser	Leu	Glu	Leu	Ala	Arg	Ala	Gln	Lys	Gln	Pro	
			20					25					30			
Glu	Gly	Ser	Asn	Thr	Pro	Pro	Thr	Leu	Ser	Gly	Val	Leu	Ala	Lys	Arg	
			35				40					45				
Lys	Arg	Val	Ile	Glu	Asn	Ala	Leu	Ser	Lys	Thr	Val	Asp	Met	Arg	Glu	
			50			55					60					
Val	Leu	Lys	His	Glu	Thr	Val	Val	Ile	Ser	Pro	Asn	Val	Met	Asp	Glu	
			65			70				75					80	
Gly	Ala	Ile	Asp	Glu	Leu	Ile	Arg	Ala	Phe	Gly	Glu	Ser	Gly	Ile	Ala	
				85					90					95		
Glu	Ser	Ala	Gln	Phe	Asp	Val										
																100

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCAGGATTGA AGGCTGGCCA CTGTGTGATT TTTGATGAGG TCCAGTTGTT TCCTCCTGGA	60
TACATCGATC TATGCTTGCT TATTATACGT AGTGATGCTT TCATTTCACT TGCCGGTGAT	120
CCATGTCAAA GCACATATGA TTCGCAAAG GATCGGGCAA TTTTGGGCGC TGAGCAGAGT	180
GACATACTTA GAATGCTTGA GGGCAAACG TATAGGTATA ACATAGAAAG CAGGAGGTTT	240
GTGAACCCAA TGTTCAATC AAGACTGCCA TGTCACCTCA AAAAGGGTTC GATGACTGCC	300
GCTTTGCTG ATTATGCAAT CTTCCATAAT ATGCATGACT TTCTCCTGGC GAGGTCAAAA	360
GGTCCTTTGG ATGCCGTTTT GGTTCAGT TTTGAGGAGA AAAAGATAGT CCAGTCCTAC	420
TTTGGAATGA AACAGCTCAC ACTCACATTT GGTGAATCAA CTGGGTTGAA TTTCAAAAAT	480

GGGGGAATTC TCATATCACA TGATTCCTTT CACACAGATG ATCGGCCGGT GGCTTACTGC	540
TTTATCTCGC TTCAGCCACA ATTTGGATTT GGTGAACATT ACAGGTCTGA GGGTGGAAG	600
TTTCCTCTCG CACTTTGCTG GCAAACCCCT CTACCATTTT TTAACAGCCA AAAGTGGGGA	660
GAATGTCATA CGAGATTGTC TCCCAGGTGA GCCTAACTTC TTCAGTGGCT TTAACGTTAG	720
CATTGGAAAG AATGAAGGTG TTAGGGAGGA GAAGTTATGT GGTGACCCAT GGTAAAAGT	780
CATGCTTTTC CTGGGTCAAG ATGAGGATTG TGAAGTTGAA GAGATGGAGT CAGAGTGCTC	840
AAATGAAGAA TGGTTTAAAA CCCACATTCC CCTGAGTAAT CTGGAGTCAA CCAGGGCTAG	900
GTGGGTGGGT AAAATGGCTT TGAAAGAGTA TCGGGAGGTG CGTTGTGGTT ATGAAATGAC	960
TCAACAATTC TTTGATGAGC ATAGGGGTGG AACTGGTGAG CAACTGAGCA ATGCATGTGA	1020
GAGGTTTGAA AGCATTACC CAAGGCATAA AGGAAATGAT TCAATAACCT TCCTTATGGC	1080
TGTCCGAAAG CGTCTCAAAT TTTCGAAGCC CCAGGTTGAA GCTGCCAAAC TGAGGCGGGC	1140
CAAACCATAT GGGAAATTCT TATTAGACTT TCCTATCCAA AATCCCATTG AAAGCCAGTC	1200
ATAATT	1206

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1284 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATTAACCCAA ATGGTAAGAT TTCCGCCTTG TTTGATATAA CCAATGAGCA CATAAGGCAT	60
GTTGAGAAGA TCGGCAATGG CCCTCAGAGC ATAAAAGTAG ATGAGTTGAG GAAGGTTAAG	120
CGATCCGCCC TTGATCTTCT TTCAATGAAT GGGTCCAAAA TAACCTATTT TCCAACTTT	180
GAGCGGGCTG AAAAGTTGCA AGGGTGCTTG CTAGGGGGCC TAACTGGTGT CATAAGTGAT	240
GAAAAGTTCA GTGATGCAAA ACCCTGGCTT TCTGGTATAT CAACTGCGGA TATAAGCCA	300
AGAGAGCTAA CTGTCGTGCT TGGCACTTTT GGGGCTGGAA AGAGTTTCTT GTATAAGAGT	360
TTCATGAAGA GATCTGAGGG AAAATTTGTA ACTTTTGTTC CCCCTAGACG AGCCTTGGCA	420
AATTCAATCA AAAATGATCT TGAAATGGAT GATGGCTGCA AAGTTGCCAA AGCAGGCAAA	480
TCAAAGAAGG AAGGGTGGGA TGAGTGACC TTTGAAGTTT TCCTTAGAAA AGTTTCTGGT	540
TTGAAAGCTG GTCATTGTGT GATTTTGTAT GAGGTTTCAGT TGTTTCCCCC TGGATACATC	600

GATCTGTGTT TACTTGTCAT ACGAAGTGAT GCTTTCATTT CACTTGCTGG TGATCCATGC	660
CAGAGCACAT ATGATTCACA GAAGGATCGA GCAATTTTGG GAGCTGAGCA GAGTGACATA	720
CTCAGACTGC TTGAAGGAAA GACATATAGG TACAACATAG AAAGCAGACG TTTTGTGAAC	780
CCAATGTTTG AATCTAGACT ACCATGTCAC TTCAAAAAGG GTTCAATGAC TGCAGCCTTT	840
GCTGATTATG CAATCTTCCA CAATATGCAT GACTTCCTCC TGGCGAGGTC AAAAGGCCCC	900
TTGGATGCTG TTCTAGTTTC CAGTTTTGAG GAGAAGAAAA TAGTCCAATC CTACTTTGGG	960
ATGAAGCAAC TCACTCTCAC ATTTGGTGAA TCAACTGGGT TGAAGTTCAA AAATGGAGGA	1020
ATTCTCATAT CACATGACTC CTTTCATACT GACGATCGAC GGTGGCTTAC TGCTTTATCT	1080
CGATTCAGCC ATAATTTGGA TTTGGTGAAC ATCACAGGTC TTGAGGGTGG AAAGTTTTCT	1140
CTCACATTTT GCTGGTAAAC CCCTTTACCA CTTTTTGACG GCTTAAAAGT GGAGAGAATG	1200
TCATACGAGA CCTGCTTCAG GTGAGCCTAA CTTCTTTTAG GGGTTCAATG TCAGCATTGG	1260
AAAAAATGG AAGGGGTTAG AGAA	1284

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CATTTTTTAAA ATTTAATCCA GTCGACTCAC CAAATGTGAG CGTAAGCTGT TTCATCCCAA	60
AGTAGGACTG GACTATTTTC TTCTCCTCAA AACTAGAAAC CAGAATGGCA TCCAAAGGAC	120
CTTTTGACCT TGCCAGGAGG AAATCATGCA TATTGTGGAA AATGGCATAA TCAGCAAAGG	180
CAGCAGTCAT TGTACCCTTT TTGAAGTGAC ATGGCAGTCG AGATTCAAAC ATTGGGTTCA	240
CAAATCTTCT GCTTTCTATG TTGTACCTAT ACGTCTTGCC TTCAAGTATT TTGAGTATGT	300
CACTCTGCTC AGCGCCCAAA ATCGCCCGAT CTTTTTGTA GTCATATGTG CTCTGACATG	360
GGTCACCAGC AAGTGAAATG AAAGCATCAC TACGTATAAT AAGCAAACAT AGATCGATGT	420
ATCCAGGGGG AAACAACTGG ACCTCATCGA AAATTACACA GTGACCAGCT TTTAGACCTG	480
CAACTTTTCT AAGGAAGACT TCAAAAGTCA CAACATCCCA TCCTTCCTTC TTTGACCTGC	540
CTGCTTTGGC AACTTTGCAG CTATCATCCA TTTCAAGATC ATTTTGTATT GAATTCGCTA	600

GAGCCCGTCT GGGGGAAACA AAAGTTACGA ATTTACCCTC AGATCTTTTC ATAAAGCTCT	660
TGTACAAAAA GCTTTTTCCT GCTCCAAATG TGCCAAGCAC AACAGTTAGC TCCCTCGGCT	720
TAATGTCAGT AGTTGATATA CCAGAAAGCC AGGGCTTTCG ATCACTGAAC TTCTCATCAC	780
TTATGACACC AGTTAGGCCT CCTAGCAGAC ACCCTTGCAA CTTTTCAGCC CGCTCAAAAC	840
TTGGGAAGTA GGTTACCTTG GACCCATTAA TTGAAAGAAG ATCAAGGGCG GATCGCTTGA	900
CCTTTCGCAA TTCATCTACT TTAATGCTCT GAGGGCCATT ACCTATCTTT TCAACATGCC	960
TTATGTGCTC ATTAGTTATG TCAAACAGAG CGGAAAACCT GCCATGTGGA TTAATCACCT	1020
CAATTTCCCC ATTTATGTCA CACTTAGCGC AAATGTCAA AGCCTCAAAG GCTTCAGCTA	1080
AGTTACATCA TGTTGAGCCT CCCCTTGGC AAAGCTCCTC AAAAATGTGG TTAGTGCTAG	1140
GCCTGCACAA TAATTAACAC ATCAACTTCA CCCTGCCAAT GCTGAACAAT ACTGTTATCA	1200
TGCAACCATC CATGGGGCAC ATGGTTGGAA TTGATTGATT TAAGGCAAAA ATCCCCACAG	1260
GGGGCATCCC CTTCCTCAAT TTCCACTGAT TCATACTCTG GCGTTATCAT ATCAACCCAA	1320
TGTGTCAAAT ACAAATAATG CAATCTCTCA TCTCCGATAA CATTTCCCCC ATTTTTTAAA	1380
AATGGTGGGG TGAAAATTGG AA	1402

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1236 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTGGTTTTTG CAACAACAGG CCCAGGTCTA TCTAAGGTTT TGGAAATGCC TCGAAGCAAG	60
AAGCAATCTA TTCTGGTTCT TGAGGGAGCC CTATCCATAG AAACGGACTA TGGCCCCAAA	120
GTTCTGGGAT CTTTGAAGT TTTCAAAGGG GATTTCACA TTAATAAAAT GGAAGAAAGT	180
TCCATCTTTG TAATAACATA CAAGGCCCCA GTTAGATCTA CTGGCAAGTT GAGGGTCCAC	240
CAATCAGAAT GCTCATTTTC TGGATCCAAG GAGGTATTGC TGGGTTGTCA GATTGAGGCA	300
TGTGCTGATT ATGATATTGA TGATTTCAT ACTTCTTTG TACCTGGTGA TGGTAATTGC	360
TTTTGGCATT CAGTTGGTTT CTTACTCAGT ACTGACGGAC TTGCTTTGAA GGCCGGCATT	420
CGTTCTTTCG TGGAGAGTGA ACGCCTGGTG AGTCCAGATC TTTCAGCCCC AACCATTCT	480
AAACAACCTGG GGGAAAATGC TTATGCCGAG AATGAGATGA TTGCATTATT TTGTATTCTGA	540

CACCATGTGA GGCTGATAGT GATTACGCCA GAGTATGAAG TCAGTTGGAA ATTTGGGGAA	600
GGTGAATGGC CCCTGTGCGG AATTCTTTGC CTTAAATCAA ATCACTTCCA ACCATGTGCC	660
CCATTGAATG GTTGCATGAT TACAGCTATT GCTTCAGCAC TTGGTAGGCG TGAAGTTGAT	720
GTGCTTAATT ATCTGTGCAG GCCTAGCACT AACCACATTT TTGAGGAGCT TTGCCAAGGG	780
GGAGGCCTCA ACATGATGTA CTTAGCTGAA GCCTTTGAGG CTTTGTGACAT TTGCGCTAAG	840
TGTGACATAA ATGGGGAAAT TGAGGTGATT AATCCACATG GCAAGTTTTC CGCTCTGTTT	900
GACATAACTA ATGAGCACAT AAGGCATGTT GAAAAGATAG GTAATGGCCC TCAGAGCATT	960
AAAGTAGATG AATTGCGAAA GGTCAAGCGA TCTGCCCTTG ATCTTCTTTC AATTAATGGG	1020
TCCAAGGTAA CCTACTTCCC AAGTTTTGAG CGGGCTGAAA AGTTGCAAGG GTGTCTGCTA	1080
GGAGGCCTAA CTGGTGTCTAT AAGTGATGAG AAAGTCAGTG ATGCAAAGCC CTGCTTTTTG	1140
GTATATCAAC TACTGACATT AAGCCGAGGG AGCTAACTGT TGTGCTTTGG CACATTTGGA	1200
GCCCGGAAAA AGCCTTTTGT ACCAAGAGCT TTATTG	1236

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GTCTAACTGG CGTTATAAGT GATGAGAAAT TCAGTGATGC AAAACCTTGG CTTTCTGGTA	60
TATCTACTAC AGATATTAAG CCAAGGGAAT TAACTGTTGT GCTTGGTACA TTTGGGGCTG	120
GGAAGAGTTT CTTGTACAAG AGTTTCATGA AAAGGTCTGA GGGTAAATTC GTAACCTTTG	180
TTTCTCCCAG ACGTGCTTTA GCAAATTCAA TCAAAAATGA TCTTGAAATG GATGATAGCT	240
GCAAAGTTGC CAAAGCAGGT AGGTCAAAGA AGGAAGGGTG GGATGTAGTA ACTTTTGAGG	300
TCTTCCTCAG AAAAGTTGCA GGATTGAAGG CTGGCCACTG TGTGATTTTT GATGAGGTCC	360
AGTTGTTTCC TCCTGGATAC ATCGATCTAT GCTTGCTTAT TATACGTAGT GATGCTTTCA	420
TTTCACTTGC CGGTGATCCA TGTCAAAGCA CATATGATTC GCAAAGGAT CGGGCAATTT	480
TGGGCGCTGA GCAGAGTGAC AACTTAGAA TGCTTGAGGG CAAAACGTAT AGGTATAACA	540
TAGAAAGCAG GAGGTTTGTG AACCCAATGT TCGAATCAAG ACTGCCATGT CACTTCAAAA	600

AGGGTTCGAT GACTGCCGCT TTCGCTGATT ATGCAATCTT CCATAATATG CATGACTTTC	660
TCCTGGCGAG GTCAAAAGGT CCTTTGGATG CCGTTTTGGT TTCCAGTTTT GAGGAGAAAA	720
AGATAGTCCA GTCCTACTTT GGAATGAAAC AGCTCACACT CACATTTGGT GAATCAACTG	780
GGTTGAATTT CAAAAATGGG GGAATTCTCA TATCACATGA TTCCTTTCAC ACAGATGATC	840
GGCGGTGGCT TACTGCTTTA TCTCGCTTCA GCCACAATT GGATTTGGTG AACATTACAG	900
GTCTGAGGTG GAAAGTTTCC TCTCGCACTT TGCTGGCAAA CCCCTCTACC ATTTTTTAAC	960
AGCCAAAAGT GGGGAGAATG TCATACGAGA TTTGCTCCCA GGTGAGCCTA ACTTCTTCAG	1020
TGGCTTTAAC GTTAGCATTG GAAAGAATGA AGGTGTTAGG GAGGAGAAGT TATGTGGTGA	1080
CCCATGGTTA AAAGTCATGC TTTTCCTGGG TCAAGATGAG GATTGTGAAG TTGAAGAGAT	1140
GGAGTCAGAG TGCTCAAATG AAGAATGGTT TAAAACCCAC ATTCCCCTGA GTAATCTGGA	1200
GTCAACCAGG GCTAGGTGGG TGGGTAAAAT GGCCTTGAAA GAGTATCGGG AGGTGCGTTG	1260
TGGTTATGAA ATGACTCAAC AATTCTTTGA TGACAT	1296

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATGTTACCA AATCCAAATT ATGGCTGAAG CGAGATAAAG CAGTAAGCCA CCGCCGATCA	60
TCTGTGTGAA AGGAATCATG TGATATGAGA ATTCCCCCAT TTTTGAAATT CAACCCAGTT	120
GATTCACCAA ATGTGAGTGT GAGCTGTTTC ATTCCAAAGT AGGACTGGAC TATCTTTTTC	180
TCCTCAAAC TGGAAACCAA AACGGCATCC AAAGGACCTT TTGACCTCGC CAGGAGAAAG	240
TCATGCATAT TATGGAAGAT TGCATAATCA GCGAAAGCGG CAGTCATTGA GCCCTTTTTC	300
AATTGACATG GCAGTCTTGA TTCGAACATT GGATTCACAA ACCTCCTGCT TTCAATGTTA	360
TACCTATACG TCTTGCCCTC AAGCAGTCTA AGTATGTCAC TCTGCTCAGC GCCCAAATT	420
GCCCGATCCT TTTGCGAATC ATATGTGCTT TGACATGGAT CACCGGCAAG TGAAATGAAA	480
GCATCACTAC GTATAATAAG CAAGCATAGA TCGATGTATC CAGGAGGAAA CAACTGGACC	540
TCATCGAAAA TCACACAGTG GCCAGCCTTC AATCCTGCAA CTTTTCTGAG GAAAACCTCA	600
AAAGTTACTA CATCCCACCC TTCCTTCTTT GACCTACCTG CTTTAGCAAC TTTGCAGCTA	660

TCATCCATTT CAAGATCATT TTTGATTGAA TTTGCTAAAG CACGTCTGGG AGAAACAAAG	720
GTTACGAATT TACCCTCAGA CCTTTTCATG AACTCTTGT ACAAGAACT CTTCCCAGCC	780
CCAAATGTAC CAAGCACGAC AGTCAACTCC CTTGGCTTAA TATCAGTAGT AGATATACCA	840
GAAAGCCAAG GTTTTGCATC ACTGAACTTC TCATCACTTA TAACGCCAGT TAGGCCCCCT	900
AGCAAAC	907

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATGCTTA TGCTGAGAAT GAGATGATTG CATTATTTTG CATCCGGCAC CATGTAAGGC	60
TTATAGTAAT AACACCGGAA TATGAAGTTA GTTGGAATT TGGGGAAAGT GAGTGGCCCC	120
TATGTGGAAT TCTTTGCCTG AGGTCCAATC ACTTCCAACC ATGCGCCCCG CTGAATGGTT	180
GCATGATCAC GGCTATTGCT TCAGCACTTG GGAGGCGTGA GGTTGATGTG TTAAATTATC	240
TGTGTAGGCC TAGCACTAAT CACATCTTTG AGGAGCTGTG CCAGGGCGGA GGGCTTAATA	300
TGATGTACTT GGCTGAAGCT TTTGAGGCCT TTGACATTTG TGCAAAGTGC GACATAAATG	360
GGGAAATTGA GGTCAATTAAC CCAAATGGCA AGATTTCCGC CTTGTTTGAT ATAATAATG	420
AGCACATAAG GCATGTTGAG AAGATCAGCA ATGGCCCTCA GAGCATAAAA ATAGATGAGT	480
TGAGGAAGGT TAAGCGATCC CGCCTTGACC TTCTTTCAAT GAATGGGTCC AAAATAACCT	540
ATTTTCCAAA CTTTGAGCGG GCTGAAAAGT TGCAAGGGTG CTTGCTAGAG GGCCTGACTG	600
GTGTCATAAG TGATGAAAAG TTCAGTGATG CAAAACCTTG GCTTTCTGGT ATATCAACTG	660
CGGATATTAA GCCAAGAGAG CTAAGTGTG TGCTTGGCAC ATTTGGTGCT GGAAAGAGTT	720
TCTTGATATA GAGTTTCATG AAGAGATCTG AAGGAAAATT TGTAACTTTT GTTCCCCTA	780
GGCGAGCTTT GGCCAATTCT ATCAAGAATG ATCTTGAAAT GGATGATGGC TGCAAAGTTG	840
CCAAAGCAGG CAAGTCAAAG AAGGAAGGGT GGGATGTGGT AACATTTGAG GTTTTCCTTA	900
GAAAAGTTTC TGGTTTGAAG GCTGGTCATT GTGTGATTTT CGATGAGGTT CAGTTGTTTC	960
CCCCTGGATA TATCGATCTA TGTTTACTTG TCATACGCAG TGATGCTTTT ATTTCACTTG	1020

CCGGTGATCC ATGCCAGAGC ACATATGATT CACAAAAGGA TCGGGCAATT TTGGGAGCTG	1080
AGCAGAGTGA CATACTCAGA TTGCTTGAAG GAAAGACGTA TAGGTACAAC ATAGAAAGCA	1140
GACGTTTTGT GAACCCAATG TTTGAATTGA GACTACCATG TCACTTCAAA AAAGGGTTCA	1200
ATGACTGCTG CCTTTGCTGA TTATGCAATC TT	1232

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCTTCAGCAC TTGGAAGGCG

20

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACACAGTGG CCAGCCT

17

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGAGGTGCGT TGTGGTTATG

20

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCCTGGCACT GCACACCC

18

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GGAGGTGACC ACATTACG

18

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CATCACGACT TGTCAAAAC C

21

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TGGGCCTCCA CTTCTTC

17

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGGGTTGCCT GAAGAT

16

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ACACCTGCTG TGAAAGC

17

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGCCAAGGTT CAGTTTG

17

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGAGGTCC AGTTGTTTCC

20

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATCCAAAGGA CCTTTTGACC

20

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTTGATGAGT ACTTGTC

17

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GCAAGGATTT GGATGGC

17